

**From:** Prasad, Sarada  
**Sent:** Friday, June 08, 2001 9:19 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** ser no. 09227854

Please perform a sequence search for the seq id no. 2 of this application.  
This is an overdue amendment I acquired. I appreciate if this can be a rush.  
thank you,

Sarada Prasad, Ph.D.  
Patent Examiner  
Art Unit 1646  
Room CM1-8B17  
Tel: 703-305-1009

KM calcium-binding protein; calcium homeostasis; cardiac muscle;  
 KM pumping capacity; myocardial cell; systolic calcium ion release;  
 KM sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;  
 KM valve defect.  
 XX  
 XX Homo sapiens.  
 OS  
 XX DE19915485-A1.  
 PN  
 XX 19-OCT-2000.  
 PD  
 XX 07-APR-1999; 99DE-1015485.  
 PF  
 XX 07-APR-1999; 99DE-1015485.  
 PR  
 XX 07-APR-1999; 99DE-1015485.  
 PA (KATU/) KATUS H A.  
 PA (REMP/) REMPPIS A.  
 PI Katus HA, Remppis A;  
 PY  
 WP1: 2000-673510/66.  
 N-PSDB: C81814.  
 XX  
 PT Composition containing S100 protein, corresponding nucleic acid or  
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency  
 XX  
 PS Claim 35; Page 22; 36pp; German.  
 XX  
 CC This invention describes a novel composition for treating primary or  
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one  
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or  
 CC fragments, or a gene transfer vector containing (II), optionally  
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding  
 CC proteins involved in calcium homeostasis, so their overexpression in  
 CC cardiac muscle will improve pumping capacity (and overall capacity) of  
 CC the heart. In cultured myocardial cells they increase the contraction and  
 CC relaxation rates associated with increased systolic calcium ion release  
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are  
 CC used to treat cardiomyopathy (CMP) where inherited or caused by  
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,  
 CC dilative CMP caused by toxic/infectious disease, cardiac disease caused  
 CC by pulmonary and/or arterial hypertension, and structural disease caused  
 CC by rhythm disorders or valve defects, generally any condition associated  
 CC with reduced contractile force. Unlike calmodulin, which is expressed  
 CC ubiquitously, (I) show tissue-specific expression and treat the  
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac  
 CC disease.  
 CC  
 XX Sequence 95 AA;  
 SO  
 Query Match 41.5%; Score 194; DB 21; Length 95;  
 Best Local Similarity 45.1%; Pred. No. 1.7e-14;  
 Matches 41; Conservative 17; Mismatches 33; Indels 0; Gaps 0;  
 QY 1 MTKLEHLEGIVNIHFQSVVRKGHPDTLSKGEKOLLTKRELANTIKNKRAVIDEIFOG 60  
 DB 1 mteletamgmildvfrsrgsgstqtlkgeikvimekelpgfigsgkdkavdkllkd 60  
 QY 61 LDANODEQVDFQEFISLVAIALKAHYHTHK 91  
 DB 61 ldangdaqvdfseeflvfaaltsachkyfek 91  
 RESULT 15  
 B45345  
 ID B45545 standard; Protein; 95 AA.  
 XX  
 AC B45545;  
 XX  
 DT 22-FEB-2001 (first entry)  
 XX  
 DE Human S100P protein.

XX  
 XX S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;  
 KM calcium-binding protein; calcium homeostasis; cardiac muscle;  
 KM pumping capacity; myocardial cell; systolic calcium ion release;  
 KM sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;  
 KM valve defect.  
 XX  
 XX Homo sapiens.  
 OS  
 XX DE19915485-A1.  
 PN  
 XX 19-OCT-2000.  
 PD  
 XX 07-APR-1999; 99DE-1015485.  
 PF  
 XX 07-APR-1999; 99DE-1015485.  
 PR  
 XX 07-APR-1999; 99DE-1015485.  
 PA (KATU/) KATUS H A.  
 PA (REMP/) REMPPIS A.  
 PI Katus HA, Remppis A;  
 PY  
 WP1: 2000-673510/66.  
 N-PSDB: C81815.  
 XX  
 DR  
 DR  
 XX  
 PT Composition containing S100 protein, corresponding nucleic acid or  
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency  
 XX  
 PS Claim 35; Page 23; 36pp; German.  
 XX  
 CC This invention describes a novel composition for treating primary or  
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one  
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or  
 CC fragments, or a gene transfer vector containing (II), optionally  
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding  
 CC proteins involved in calcium homeostasis, so their overexpression in  
 CC cardiac muscle will improve pumping capacity (and overall capacity) of  
 CC the heart. In cultured myocardial cells they increase the contraction and  
 CC relaxation rates associated with increased systolic calcium ion release  
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are  
 CC used to treat cardiomyopathy (CMP) where inherited or caused by  
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,  
 CC dilative CMP caused by toxic/infectious disease, cardiac disease caused  
 CC by pulmonary and/or arterial hypertension, and structural disease caused  
 CC by rhythm disorders or valve defects, generally any condition associated  
 CC with reduced contractile force. Unlike calmodulin, which is expressed  
 CC ubiquitously, (I) show tissue-specific expression and treat the  
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac  
 CC disease.  
 CC  
 XX Sequence 95 AA;  
 SO  
 Query Match 41.5%; Score 194; DB 21; Length 95;  
 Best Local Similarity 45.1%; Pred. No. 1.7e-14;  
 Matches 41; Conservative 17; Mismatches 33; Indels 0; Gaps 0;  
 QY 1 MTKLEHLEGIVNIHFQSVVRKGHPDTLSKGEKOLLTKRELANTIKNKRAVIDEIFOG 60  
 DB 1 mteletamgmildvfrsrgsgstqtlkgeikvimekelpgfigsgkdkavdkllkd 60  
 QY 61 LDANODEQVDFQEFISLVAIALKAHYHTHK 91  
 DB 61 ldangdaqvdfseeflvfaaltsachkyfek 91  
 Search completed: June 8, 2001, 15:03:24  
 Job time: 24 sec

KW calcium-binding protein; calcium homeostasis; cardiac muscle;  
 KW pumping capacity; myocardial cell; systolic calcium ion release;  
 KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;  
 KW valve defect.  
 OS Homo sapiens.  
 XX DE19915485-A1.  
 XX PD 19-OCT-2000.  
 XX PF 07-APR-1999; 99DE-1015485.  
 XX PR 07-APR-1999; 99DE-1015485.  
 XX PA (KATU/) KATIS H A.  
 XX PA (REMP/) REMPPIS A.  
 XX PI Katus HA, Remppis A;  
 WP1: 2000-673510/66.  
 LN N-PSDB; C81809.

Composition, containing S100 protein, corresponding nucleic acid or vector, useful for treating cardiomyopathy and cardiac insufficiency  
 PS Claim 35; Page 16-17; 36pp; German.

This invention describes a novel composition for treating primary or secondary cardiomyopathy or cardiac insufficiency contains at least one S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or fragments, or a gene transfer vector containing (II), optionally formulated with auxiliaries and/or carriers. (I) are calcium-binding proteins involved in calcium homeostasis, so their overexpression in cardiac muscle will improve pumping capacity (and overall capacity) of the heart. In cultured myocardial cells they increase the contraction and relaxation rates associated with increased systolic calcium ion release from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are used to treat cardiomyopathy (CMP) where inherited or caused by spontaneous mutations and ischemic CMP caused by arteriosclerosis, dilative CMP caused by toxic/infectious disease, cardiac disease caused by pulmonary and/or arterial hypertension, and structural disease caused by rhythm disorders or valve defects, generally any condition associated with reduced contractile force. Unlike calmodulin, which is expressed ubiquitously, (I) show tissue-specific expression and treat the underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac disease.

Sequence 114 AA:

Query Match 45.8%; Score 214.5; DB 21; Length 114;  
 Best Local Similarity 46.7%; Pred. No. 1.1e-16;  
 Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;  
 QY 1 MTKLEHLGIVNIFHOYSVRKGFDTLSKGLKQLTRELANTI-KNIKRAVIDEIRQ 59  
 Db 5 msqlemnietlntfngysvkighpdtlmgelkelyrkdqgflkknknevlehm 64  
 QY 60 GLDANODEQVDFEISLVAIALKAHHTK 91  
 Db 65 dltndakqjstfeefimarlwashekme 96

RESULT 13

ID Y87637 standard; Protein; 114 AA.  
 AC Y87637;  
 DT 04-AUG-2000 (first entry)  
 XX Human calcium-binding protein #2.  
 DE

XX Calcium-binding protein; granule release; calgranulin; human;  
 KW vascular membrane growth; adult respiratory distress syndrome;  
 KW acute myocardial infarction; ischemic reperfusion disorder;  
 KW glomerulonephritis; rheumatoid arthritis; chronic bronchitis;  
 KW cerebral vascular disorder; asthma; peripheral circulation disturbance;  
 KW angina pectoris; hypertension; multiple sclerosis.  
 OS Homo sapiens.  
 XX WO200018970-A1.  
 XX PD 06-APR-2000.  
 XX PF 28-SEP-1999; 99WO-JP05302.  
 XX PR 29-SEP-1998; 98JP-0274574.  
 XX PA (ASAH) ASAH KASEI KOGYO KK.  
 XX PI Seto M, Fukuda K;  
 WP1: 2000-293189/25.  
 LN N-PSDB; A11970.

Controlling the release of granules from cell system using activated calgranulin for screening substances for granule activating or inhibiting activity  
 PS Disclosure; Page 39-40; 42pp; Japanese.

This invention describes a novel method for controlling the release of granules by treating a cell system to increase or decrease activated calgranulin to enhance or depress the release of granules. Calgranulin is a calcium binding protein and can be used for controlling the release of granules from a cell system e.g. those involved with the inhibition of vascular membrane growth. Vascular membrane growth is associated with e.g. adult respiratory distress syndrome, acute myocardial infarction due to ischemic reperfusion disorders, glomerulonephritis, rheumatoid arthritis, chronic bronchitis, cerebral vascular disorders, asthma, peripheral circulation disturbance, angina pectoris, hypertension and multiple sclerosis. The new method is used for screening substances for their ability to activate or inhibit the release of granules. This sequence represents a human calcium-binding protein which is described in the method of the invention.

Sequence 114 AA:

Query Match 45.8%; Score 214.5; DB 21; Length 114;  
 Best Local Similarity 46.7%; Pred. No. 1.1e-16;  
 Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;  
 QY 1 MTKLEHLGIVNIFHOYSVRKGFDTLSKGLKQLTRELANTI-KNIKRAVIDEIRQ 59  
 Db 5 msqlemnietlntfngysvkighpdtlmgelkelyrkdqgflkknknevlehm 64  
 QY 60 GLDANODEQVDFEISLVAIALKAHHTK 91  
 Db 65 dltndakqjstfeefimarlwashekme 96

RESULT 14

ID B45544 standard; Protein; 95 AA.  
 AC B45544;  
 DT 22-FEB-2001 (first entry)  
 XX Human S100B protein.  
 DE S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;  
 KW

00 65 atadnauqrsteel llllllall lwashnekmlle 90

SW100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;

[illegible]

SQ Sequence 91 AA;

## Query Match

Best Local Similarity 70.3%; Score 337; DB 20; Length 91;  
 Matches 64; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 2 TRKEEHLGIVNTHQSVRKGFHPTLSKGLKQLTKELANTIKNIKRAVIDEIQGL 61  
 DB 1 tleedhleglntfhgsvrvghydtlkrklqtltkelpnltnktgdqtdkrlfqn 60  
 OY 62 DANODEQVDFQEFISLVAIALKAHYHTHKE 92  
 DB 61 dangdeqvsfkefvvltvtdltahdnhke 91

## RESULT 6

W03563 standard; Protein; 92 AA.

W03563;

01-MAY-1997 (first entry)

Calcium binding protein CAAFL.

KW Intracellular signal transduction; squamous epithelial cell; neutrophil;  
 KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;  
 KW squamous cell carcinoma; skin; oesophagus; CAAFL; lung; blood disease.  
 OS Bos taurus.

EP731166-A2.

11-SEP-1996.

04-DEC-1995; 95EP-0119045.

06-MAR-1995; 95JP-0070468.

06-MAR-1995; 95JP-0045564.

(HITO/) HITOMI J.

(TOFU) TONEN CORP.

Hitomi J, Kimura T, Yamaguchi K, Yamamura T;

WPI: 1996-403989/41.

N-PSDB: T39345.

New human or bovine calcium binding protein and related nucleic acid

- is a marker for inflammation, neoplasia, skin and blood diseases

Claim 1: Page 21; 36pp; English.

This sequence represents the CAAFL calcium-binding protein isolated from  
 CC bovine amniotic fluid. CAAFL belongs to the S100 protein family, which  
 CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion  
 CC concentration is one of the key factors for intracellular signal  
 CC transduction. The calcium signals are transduced by various  
 CC calcium-binding proteins, such as the protein encoded by this sequence.  
 CC CAAFL is normally expressed in squamous epithelial cells, neutrophils and  
 CC macrophages, but atypical epithelial cells are negative for CAAFL and  
 CC overexpression is observed in several types of cancer cells and  
 CC neutrophils/macrophages infiltrating cancerous lesions. Detection of  
 CC CAAFL (using antibodies in usual immunoassays) can be used to diagnose  
 CC (or monitor) inflammation, neoplasia (particularly squamous cell  
 CC carcinoma of the skin, oesophagus, lung and cervix), and skin and blood  
 CC diseases.

SQ Sequence 92 AA;

Query Match 68.2%; Score 319; DB 17; Length 92;  
 Best Local Similarity 66.3%; Pred. No. 1.8e-28;  
 Matches 61; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

OY 1 MKRLEHLEGIYNTFHQSVRKGFHPTLSKGLKQLTKELANTIKNIKRAVIDEIQGL 60  
 DB 1 mklechleglntfhgsvrvghydtlkrklqtltkelpnltnktgdqtdkrlfqn 60  
 OY 61 LDANODEQVDFQEFISLVAIALKAHYHTHKE 92  
 DB 61 ldkdkgavsfkefvvltvtdltahdnhke 92

## RESULT 7

Y90764 standard; Protein; 90 AA.

Y90764;

18-AUG-2000 (first entry)

Bovine corneal antigen (B-COA) acid sequence SEQ ID NO:3.

KW Bovine; EN-RAGE; extracellular novel RAGE binding protein;  
 KW receptor for advanced glycation endproduct; inflammation; inhibition;  
 KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;  
 KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;  
 KW autoimmune disorder; inflammatory disorder.

Bos taurus.

WO200020621-A1.

13-APR-2000.

06-OCT-1999; 99WO-US23303.

06-OCT-1998; 98US-0167705.

05-MAR-1999; 99US-0263312.

(UYCO) UNIV COLUMBIA NEW YORK.

Schmidt AM, Stern D;

WPI: 2000-303794/26.

New human EN-RAGE (extracellular novel receptor for advanced glycation

end products) peptide, useful for identifying anti-inflammatory

compounds that inhibit its interaction with RAGE -

Claim 2: Page 41; 132pp; English.

The present invention describes an isolated human EN-RAGE (extracellular  
 CC novel receptor for advanced glycation end products) peptide (PI). The  
 CC EN-RAGE peptide binds to RAGE which is a member of the immunoglobulin  
 CC superfamily of cell-surface molecules. A compound capable of inhibiting  
 CC the interaction of EN-RAGE with RAGE is useful for the suppression of  
 CC inflammation resulting from systemic lupus erythematosus, inflammatory  
 CC lupus nephritis, septic shock, endotoxaemia, or an autoimmune or  
 CC inflammatory disorder in which the recruitment of EN-RAGE containing  
 CC inflammatory cells occurs. The compound is also useful for the treatment  
 CC of systemic lupus erythematosus, inflammatory lupus nephritis in a  
 CC subject. The human EN-RAGE peptide is useful for identifying compounds  
 CC that inhibit its interaction with RAGE. The present sequence represents  
 CC the bovine corneal antigen which shows homology to the human EN-RAGE  
 CC N-terminal amino acid sequence.

SQ Sequence 90 AA;

Query Match 66.0%; Score 309; DB 21; Length 90;

Best Local Similarity 65.6%; Pred. No. 2.3e-27;  
 Matches 59; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

CC dilative CMP caused by toxic/infectious disease, cardiac disease caused  
 CC by pulmonary and/or arterial hypertension, and structural disease caused  
 CC by rhythm disorders or valve defects, generally any condition associated  
 CC with reduced contractile force. Unlike calmodulin, which is expressed  
 CC ubiquitously, (1) show tissue-specific expression and treat the  
 CC underlying defect in the sarcolemmal reticulum (SR) that causes cardiac  
 CC disease.  
 CC XX  
 SQ Sequence 92 AA;

Query Match 100.0%; Score 468; DB 21; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 4,4e-45;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTKLEHLEGIIVNFHGYSRKGFHFLSKGLKQLTKRELANTIKIRKAVIDEIFQG 60  
 DB 1 mtkleehlegiivnfhgyssvrgkghfclskglkqltkrelantikirkavideifqg 60

61 LDANODEVDFOEFISLVAIALKAHYTHKE 92  
 DB 61 ldanodevdfgefislvalaalkaahythke 92

RESULT 4  
 W01826  
 ID W01826 standard; Protein; 91 AA.  
 AC W01826;  
 DT 16-OCT-1997 (first entry)  
 XX Component of bioactive metal RNA polypeptide.  
 DE Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;  
 KW angiogenesis; vascular state; mammalian tissue; transfer; cell;  
 KM genetic information; selective; alteration; nucleic acid content;  
 KW leukocyte; pig; monocyto-CURNP.  
 XX  
 OS Sus scrofa.  
 XX  
 PN DE19628895-A1.  
 PD 23-JAN-1997.  
 XX  
 PF 17-JUL-1996; 96DE-1028895.  
 XX  
 PE 18-AUG-1995; 95DE-1030500.  
 XX  
 PI 17-JUL-1995; 95DE-1025992.  
 XX  
 PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEMANDTEN.  
 XX  
 PI Hellmeyer IMG, Kieseletter S, Logemann E, Wissler JH;  
 XX  
 DR WPI: 1997-088586/09.  
 DR N-PSDB; T62569.  
 XX  
 PT Bioactive metal RNA polypeptide - useful for modulating  
 PT angiogenesis, etc.  
 XX  
 PS Claim 1; Page 15; 16pp; German.  
 XX  
 CC A novel bioactive metal RNA polypeptide (RNP) has a RNA component  
 CC including the sequence T62568 and a polypeptide component having  
 CC the sequence W01826, which is encoded by T62569. The RNP, or  
 CC anti-RNP immunoglobulins, can be used to modulate and/or analyse  
 CC angiogenesis and the vascular state of mammalian tissue, transfer  
 CC genetic information in cells and selectively alter the nucleic  
 CC acid content of cells.  
 CC Leukocytes from pig's blood were cultured in medium, and the  
 CC supernatant treated with NH4 sulphate at 35, 45 and 90% saturation  
 CC to precipitate protein fractions. The residual supernatant was  
 CC diluted to 45% NH4 sulphate saturation and concentrated by

CC ultrafiltration using a 0.5 kD membrane. The retentate was purified  
 CC to give 8 mg of product described as monocyto-CURNP.  
 CC XX  
 SQ Sequence 91 AA;

Query Match 70.9%; Score 332; DB 18; Length 91;  
 Best Local Similarity 70.3%; Pred. No. 6,4e-30;  
 Matches 64; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 2 TKLEHLEGIIVNFHGYSRKGFHFLSKGLKQLTKRELANTIKIRKAVIDEIFQGL 61  
 DB 1 tkleehlegiivnfhgyssvrgkghfclskglkqltkrelantikirkavideifqgl 60

QY 62 DANODEVDFOEFISLVAIALKAHYTHKE 92  
 DB 61 danodevdfgefislvalaalkaahythke 91

RESULT 5  
 W93819  
 ID W93819 standard; peptide; 91 AA.  
 AC W93819;  
 DT 21-JUN-1999 (first entry)  
 XX  
 DE Angiotropin related protein derived peptide.  
 XX  
 KW Angiotropin related protein; ARP; ternary complex; S100 protein;  
 KW copper-containing ribonucleoprotein; copper; cell selective;  
 KW morphogenic action; blood capillary endothelial cell; confluent;  
 KW non-mitogenic induction; cell phenotype; three-dimensional organoid;  
 KW spatiotemporal supracellular organisation; chemotropic; blood vessel;  
 KW tissue neovascularisation; angiogenesis modulation.  
 XX  
 OS Synthetic.  
 XX  
 PN DE19811047-C1.  
 PD 15-APR-1999.  
 XX  
 PF 13-MAR-1998; 98DE-1011047.  
 XX  
 PR 13-MAR-1998; 98DE-1011047.  
 XX  
 PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEMANDTEN.  
 XX  
 PI Brunner H, Kieseletter S, Koch-Pelster B, Kuhn E;  
 XX  
 DR WPI: 1999-216114/19.  
 DR  
 XX  
 PT Copper-containing ribonucleoproteins - useful for modulating  
 PT angiogenesis  
 XX  
 PS Disclosure; Page 2; 16pp; German.  
 XX  
 CC This invention describes novel copper-containing ribonucleoproteins  
 CC which are ternary complexes of an S100 protein, copper ions, and  
 CC RNA comprising the following consensus sequence or its complement  
 CC GGAAAUUNNNUNUUAUGN1-6CCUNNUUNNNNNNAANA0-1UAAACAUN0-5CUUNAGNO-  
 CC 13AGAA-AUN0-16UUNACAG where N = G, A, U or C. The ribonucleoproteins are  
 CC stated to have the following properties (1) cell-selective morphogenic  
 CC action in vitro on isolated primary and/or cloned blood capillary  
 CC endothelial cells in culture for the non-mitogenic induction of the  
 CC change in cell phenotype from the confluent state, for non-mitogenic  
 CC alteration of the spatiotemporal supracellular organisation of cells;  
 CC into three-dimensional organoid, capillary-like structures in culture;  
 CC (2) a specific chemotropic action on blood vessels in vivo; (3) induction  
 CC of directional growth of blood vessels in vivo and (4) induction of  
 CC neovascularisation of tissues through directed ingrowth of blood vessels.  
 CC Their use for modulating angiogenesis is claimed.  
 CC XX

PT New human or bovine calcium binding protein and related nucleic acid  
 PT - is a marker for inflammation, neoplasia, skin and blood diseases  
 XX  
 PS Claim 1; Page 24; 36pp; English.  
 CC This sequence represents the CAAPI calcium-binding protein isolated from  
 CC human amniotic fluid. CAAPI belongs to the S100 protein family, which  
 CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion  
 CC concentration is one of the key factors for intracellular signal  
 CC transduction. The calcium signals are transduced by various  
 CC calcium-binding proteins, such as this protein. CAAPI is normally  
 CC expressed in squamous epithelial cells, neutrophils and macrophages, but  
 CC atypical epithelial cells are negative for CAAPI and overexpression is  
 CC observed in several types of cancer cells and neutrophils/macrophages  
 CC infiltrating cancerous lesions. Detection of CAAPI (using antibodies in  
 CC usual immunassays) can be used to diagnose (or monitor) inflammation,  
 CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,  
 CC lung and cervix), and skin and blood diseases.  
 CC  
 SQ Sequence 92 AA;  
 Query Match 100.0%; Score 468; DB 17; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 4,4e-45;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MKTLEHLEGIYNIHFQYSVRKGHPDTLSKGLKOLLTKELANTIKNKAVIDEIFQG 60  
 DB 1 mtkleehlegiynifhgyvsvrkghdtlskglkqlltkelantlknkxkavideifg 60  
 OY 61 LDANDEQYDFOEFISLVAIALKAHHTHKE 92  
 DB 61 ldanqedydfgefislvalkaahhthke 92  
 RESULT 2  
 W24137 ID W24137 standard; Protein: 92 AA.  
 AC W24137;  
 DT 28-JAN-1998 (first entry)  
 DE Human chemotactic cytokine I.  
 DE Human chemotactic cytokine I.  
 KW Chemotactic cytokine; tumour; autoimmune disease; antagonist;  
 KW agonist.  
 XX Homo sapiens.  
 W09723640-A1.  
 PD 03-JUL-1997.  
 PF 26-DEC-1995; 95WO-US16871.  
 PR 26-DEC-1995; 95WO-US16871.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Alfonso P, Gentz R, Ni J, Su JY, Yu G;  
 DR NPI: 1997-351075/32.  
 DR N-PSDB; T85774.  
 PT DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,  
 PT chronic infection, leukaemia, etc.  
 PS Claim 12; Pages 48-49; 64pp; English.  
 CC This is a human chemotactic cytokine I polypeptide. The encoding  
 CC polynucleotide, along with a vector and a host cell can be used for the  
 CC recombinant production of the chemotactic cytokine. Cytokine agonists

CC and antagonists can be used for the treatment of a patient requiring a  
 CC chemotactic cytokine I and for the treatment of a patient requiring the  
 CC inhibition of a chemotactic cytokine I polypeptide, respectively. The  
 CC chemotactic cytokine is used to treat tumours, chronic infection,  
 CC leukaemia and T-cell mediated autoimmune diseases.  
 CC  
 SQ Sequence 92 AA;  
 Query Match 100.0%; Score 468; DB 18; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 4,4e-45;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MKTLEHLEGIYNIHFQYSVRKGHPDTLSKGLKOLLTKELANTIKNKAVIDEIFQG 60  
 DB 1 mtkleehlegiynifhgyvsvrkghdtlskglkqlltkelantlknkxkavideifg 60  
 OY 61 LDANDEQYDFOEFISLVAIALKAHHTHKE 92  
 DB 61 ldanqedydfgefislvalkaahhthke 92  
 RESULT 3  
 B45542 ID B45542 standard; Protein: 92 AA.  
 AC B45542;  
 DT 22-FEB-2001 (first entry)  
 DE Human S100A12 protein.  
 DE S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;  
 KW calcium-binding protein; calcium homeostasis; cardiac muscle;  
 KW pumping capacity; myocardial cell; systolic calcium ion release;  
 KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;  
 KW valve defect.  
 XX Homo sapiens.  
 OS  
 PN DE19915485-A1.  
 PD 19-OCT-2000.  
 PF 07-APR-1999; 99DE-1015485.  
 PR 07-APR-1999; 99DE-1015485.  
 PA (KATU/) KATUS H A.  
 PA (REMP/) REMPPIS A.  
 PI Katus HA, Remppis A;  
 DR WPI: 2000-673510/66.  
 DR N-PSDB; C81812.  
 PT Composition containing S100 protein, corresponding nucleic acid or  
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency  
 PS Claim 35; Page 20; 36pp; German.  
 CC This invention describes a novel composition for treating primary or  
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one  
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or  
 CC fragments, or a gene transfer vector containing (II), optionally  
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding  
 CC proteins involved in calcium homeostasis, so their overexpression in  
 CC cardiac muscle will improve pumping capacity (and overall capacity) of  
 CC the heart. In cultured myocardial cells they increase the contraction and  
 CC relaxation rates associated with increased systolic calcium ion release  
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are  
 CC used to treat cardiomyopathy (CMP) where inherited or caused by  
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2001, 15:03:00 ; Search time 18.53 Seconds

(Without alignments)  
283.811 Million cell updates/sec

Title: US-09-227-854-2

Sequence: 1 MTKLEHLEGIIVIFHOQSV.....ETSLVAIALKAHHTHKE 92

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 390729 seqs, 57163235 residues

11 number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

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1: A.Geneseq_0401:*
2: /SID6/gcgdata/geneseq/geneseq/AA1980.DAT:*
3: /SID6/gcgdata/geneseq/geneseq/AA1981.DAT:*
4: /SID6/gcgdata/geneseq/geneseq/AA1982.DAT:*
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6: /SID6/gcgdata/geneseq/geneseq/AA1984.DAT:*
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21: /SID6/gcgdata/geneseq/geneseq/AA1999.DAT:*
22: /SID6/gcgdata/geneseq/geneseq/AA2000.DAT:*
23: /SID6/gcgdata/geneseq/geneseq/AA2001.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	100.0	92	17	W03564
2	468	100.0	92	18	W21137
3	468	100.0	92	21	B45542
4	332	70.9	91	18	W01826
5	332	70.9	91	20	W3819
6	319	68.2	92	17	W03563
7	309	66.0	90	21	Y90764
8	309	66.0	90	21	Y90765
9	214.5	45.8	114	18	W17062
10	214.5	45.8	114	19	W60178
11	214.5	45.8	114	20	Y48615

12	214.5	45.8	114	21	B45539	Human S100A9 prote
13	214.5	45.8	114	21	Y87637	Human S100B protei
14	194	41.5	95	21	B45544	Human S100P protei
15	194	41.5	95	21	B45545	Human S100P protei
16	189	40.4	50	21	Y90763	Human EN-RAGE-N-te
17	182	38.9	91	19	W46607	Human brain protei
18	170	36.3	74	21	G01409	Human secreted pro
19	161.5	34.5	94	21	B45531	Human S100A1 prote
20	158	33.8	93	18	W17061	Human multitrang re
21	158	33.8	93	19	W60177	Human calprotectin
22	158	33.8	93	21	B45538	Human S100A8 prote
23	158	33.8	93	21	Y87636	Human calcium-bind
24	157.5	33.7	101	13	R20560	Human mts-1 protei
25	157.5	33.7	101	16	R80453	Human mts-1 protei
26	157.5	33.7	101	21	B37432	Human mts-1. Homo
27	157.5	33.7	101	21	B45534	Human S100A4 prote
28	157	33.5	105	21	B45541	Human S100A11 prot
29	157	33.5	134	21	B58356	Lung cancer associ
30	154	32.9	89	13	R23429	Murine CP-10. Mus
31	153.5	32.8	97	13	R26406	Sequence of the cl
32	153.5	32.8	97	13	R27058	Sequence of small
33	153.5	32.8	97	21	B45532	Human S100A2 prote
34	147.5	31.5	90	20	Y29553	Human lung tumour
35	147.5	31.5	90	21	B45536	Human S100A6 prote
36	147.5	31.5	90	21	B44476	Human lung tumour-
37	146	31.2	110	21	B45535	Human S100A5 prote
38	142.5	30.4	90	21	Y57068	Calbindin chain B
39	137.5	29.4	98	18	W27152	Human chemotactic
40	137.5	29.4	98	20	W82409	Human S100P2 prote
41	137.5	29.4	98	21	B45543	Human S100A13:prot
42	137.5	29.4	98	21	B07950	Amino acid sequenc
43	132	28.2	30	16	R85169	Bovine serum hepar
44	127.5	27.2	97	21	B45540	Human S100A10 prot
45	127.5	27.2	97	21	Y93605	Protein encoded by

#### ALIGNMENTS

RESULT	1	
ID	W03564	standard; Protein; 92 AA.
XX		
AC	W03564;	
XX		
DT	01-MAY-1997	(first entry)
XX		
DE	Calcium binding protein CAAFI.	
KW	Calcium binding protein; human; amniotic fluid; S100 protein family;	
KW	intracellular signal transduction; squamous epithelial cell; neutrophil;	
KW	macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;	
KW	squamous cell carcinoma; skin; oesophagus; CAAFI; lung; blood disease.	
XX		
OS	Homo sapiens.	
XX		
PN	EP731166-A2.	
XX		
PD	11-SEP-1996.	
XX		
PF	04-DEC-1995;	95EP-0119045.
XX		
PR	06-MAR-1995;	95JP-0070468.
XX		
PR	06-MAR-1995;	95JP-0045564.
XX		
PA	(HITOMI) HITOMI J.	
XX	(TOFU) TONEN CORP.	
PI	HITOMI J, Kimura T, Yamaguchi K, Yamamura T;	
XX		
DR	WPI: 1996-403989/41.	
XX	N-PSDB; T39346.	

Fri Jun 8 15:09:52 2001

us-09-227-854-2.rpr

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[illegible]

Search completed: June 8, 2001, 15:03:57  
Job time: 52 sec

R:Presland, R.B.; Haydock, P.V.; Fleckman, P.; Nirunaksiri, W.; Dale, B.A.  
 J. Biol. Chem. 267, 23772-23781, 1992  
 A:Title: Characterization of the human epidermal profilaggrin gene. Genomic organization  
 A:Reference number: A45135; MIM:93054736  
 A:Accession: A45135  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-591 <PRE>  
 A:Cross-references: GB:L01089; GB:M90967; NID:9190408; PIDN:AAA60177.1; PID:9553621  
 A:Note: Sequence extracted from NCBI backbone (NCBIRP:118773)  
 C:Genetics:  
 A:Gene: GDB:FIG  
 A:Cross-references: GDB:119912; OMIM:135940  
 A:Map position: 1q21-1q21  
 C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology  
 C:Keywords: EF hand; epidermis; polymorphism; tandem repeat  
 F:49-81/Domain: calmodulin repeat homology <EF2>

Query Match 35.7%; Score 168; DB 2; Length 591;  
 Best Local Similarity 39.1%; Pred. No. 1.1e-07;  
 Matches 36; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

DB 1 MTKLEBHEGIVNFHQYSVRKGFHPTLSKGLKOLTKELANTIKNKAKAVIDEIFQG 60  
 1 MTKLEBHEGIVNFHQYSVRKGFHPTLSKGLKOLTKELANTIKNKAKAVIDEIFQG 60  
 DB 61 LDANODEQVDQFQFISLVATLAAHYHTRKE 92  
 61 LDIDHNKKIDFTEFLMVFLLAQAYESTRKE 92

## RESULT 14

caigizarin - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext\_change 21-Jul-2000  
 C:Accession: J01300; P00243; B41004  
 R:Matanabe, M.; Ando, Y.; Todoroki, H.; Minami, H.; Hidaka, H.  
 Biochem. Biophys. Res. Commun. 181, 644-649, 1991  
 A:Title: Molecular cloning and sequencing of a cDNA clone encoding a new calcium binding  
 A:Reference number: J01300; MIM:92095968  
 A:Accession: J01300  
 A:Molecule type: mRNA  
 A:Residues: 1-102 <MAT>  
 A:Cross-references: GB:D10586; GB:D90531; NID:9217745; PIDN:BA01443.1; PID:9217746  
 A:Accession: P00243  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 25-49/53-62 <MAT2>  
 A:Experimental source: lung  
 R:Todoroki, H.; Kobayashi, R.; Matanabe, M.; Minami, H.; Hidaka, H.  
 J. Biol. Chem. 266, 18668-18673, 1991  
 A:Title: Purification, characterization, and partial sequence analysis of a newly identified  
 A:Reference number: A41004; MIM:92011625  
 A:Accession: B41004  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 25-49/53-58, 'Y', 60-62 <TOD>  
 C:Superfamily: S-100 protein; calmodulin repeat homology  
 C:Keywords: calcium binding; EF hand  
 F:9-43/Domain: calmodulin repeat homology <EF1>  
 F:52-84/Domain: calmodulin repeat homology <EF2>

Query Match 35.7%; Score 167; DB 1; Length 102;

Best Local Similarity 40.0%; Pred. No. 2.1e-08;  
 Matches 34; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

DB 2 TKLEBHEGIVNFHQYSVRKGFHPTLSKGLKOLTKELANTIKNKAKAVIDEIFQG 61  
 1 TKLEBHEGIVNFHQYSVRKGFHPTLSKGLKOLTKELANTIKNKAKAVIDEIFQG 61  
 DB 5 TETERCESLIAVFOKAGKGVSVTLSTFELSMTELAFTKOKDGVLDPMKKL 64  
 5 TETERCESLIAVFOKAGKGVSVTLSTFELSMTELAFTKOKDGVLDPMKKL 64  
 QY 62 DANODEQVDQFQFISLVATLAAHYHTRKE 96  
 62 DANODEQVDQFQFISLVATLAAHYHTRKE 96

DB 65 DLNSDGLDQFERFLNLIGGLAVACH 89  
 65 DLNSDGLDQFERFLNLIGGLAVACH 89

## RESULT 15

S06207

calvasculin - mouse

N:Alternate names: calcium-binding protein mtel; calcium-binding protein pEL98; pla

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #ext\_change 20-Jun-2000

C:Accession: S06207; JH0097; S07981; A26803; A4141; I46674

R:Edralidze, A.; Tulchinsky, E.; Grigorian, M.; Afanasyeva, A.; Senin, V.; Revazova,

Genes Dev. 3, 1086-1093, 1989

A:Title: Isolation and characterization of a gene specifically expressed in differ

A:Reference number: S06207; MIM:89378739

A:Accession: S06207

A:Molecule type: mRNA

A:Residues: 1-101 <EBR>

A:Cross-references: EMBL:X16190; NID:954926; PIDN:CAA34316.1; PID:954927

R:Tulchinsky, E.M.; Grigorian, M.S.; Edralidze, A.K.; Mlishina, N.I.; Lukanidin, E.

Gene 87, 219-223, 1990

A:Title: Structure of gene mtel, transcribed in metastatic mouse tumor cells.

A:Reference number: JH0097; MIM:90236313

A:Accession: JH0097

A:Molecule type: DNA

A:Residues: 1-101 <TUL>

A:Cross-references: GB:M36578; GB:M36579

A:Experimental source: liver

R:Tulchinsky, B.

Submitted to the EMBL Data Library, August 1989

A:Reference number: S07981

A:Accession: S07981

A:Molecule type: DNA

A:Residues: 1-47, 'VSGSXFG', 56-57, 'RTDEAA', <TUL>

A:Cross-references: EMBL:X16094; NID:953249; PIDN:CAA344224.1; PID:953250

R:Jackson-Grusby, L.L.; Swiergel, J.; Linzer, D.I.H.

Nucleic Acids Res. 15, 6677-6690, 1987

A:Title: A growth-related mRNA in cultured mouse cells encodes a placental calcium

A:Reference number: A26803; MIM:87316927

A:Accession: A26803

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-101 <JAC>

A:Cross-references: GB:X05835; NID:950310; PIDN:CAA29282.1; PID:950311

R:Goto, K.; Endo, H.; Fujiyoshi, T.

J. Biochem. 103, 48-53, 1988

A:Title: Cloning of the sequences expressed abundantly in established cell lines: I

A:Reference number: A41411; MIM:88198109

A:Accession: A41411

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-101 <GOT>

A:Cross-references: GB:D00208; NID:9220569; PIDN:BA00148.1; PID:9220570

R:Tulchinsky, E.; Kramerov, D.; Ford, H.L.; Reshetnyak, E.; Lukanidin, E.; Zain, S.

Oncogene 8, 79-86, 1993

A:Title: Characterization of a positive regulatory element in the mtel gene.

A:Reference number: I46674; MIM:93141279

A:Accession: I46674

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-47, 'VSGSXFG', 48-54 <RES>

A:Cross-references: EMBL:X16094; NID:953249; PIDN:CAA344224.1; PID:953250

C:Comment: Gene mtel is expressed in metastatic cells.

C:Genetics:

A:Gene: mtel

A:Introns: 47/3

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: calcium binding; cancer; EF hand

F:7-41/Domain: calmodulin repeat homology <EF1>

F:50-82/Domain: calmodulin repeat homology <EF2>

F:18,21,23,26,31/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted  
F:61,63,65,67,72/Binding site: calcium (Asp, Asp, Glu, Glu, Glu) #status predicted

## Query Match

Best Local Similarity 39.5%; Score 185; DB 1; Length 91;  
Matches 33; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

OY 2 TKLEHLEGIYINIFHOYSVRKGFHDTLSKGLKQLTKELANTIKNIKDKAVIDEIFOG 61

DB 1 SELEAAVALIDVFHOYSRGEDKHKLSKELINELSHLEEKEDVAVKVEL 60

OY 62 DANODEQVDFEFLISVAIALKAAH 86

DB 61 DSDGDGEDDFEFMAFAMITACH 85

## RESULT 10

JN0686

calgranulin B - rat

Species: Rattus norvegicus (Norway rat)  
Date: 03-May-1994 #sequence\_revision 23-May-1997 #text\_change 22-Jun-1999

C:Accession: JN0686

R:Imamichi, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.

Biochem. Biophys. Res. Commun. 194, 819-825, 1993

A:Title: Expression and cloning of migration inhibitory factor-related protein (MRP) 8 at

A:Reference number: JN0685; MUID:93343942

A:Accession: JN0686

A:Molecule type: mRNA

A:Residues: 1-113 <IWA>

A:Cross-references: GB:L18948; NID:g488156; PIDN:AAA18214.1; PID:g488157

C:Genetics:

A:Gene: MRP14

C:Complex: heterodimer and higher complexes with calgranulin A

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; F

F:2-113/Product: calgranulin B #status predicted <MAT>

F:11-45/Domain: calmodulin repeat homology <EP1>

F:55-87/Domain: calmodulin repeat homology <EP2>

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

F:80-91/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 38.6%; Score 180.5; DB 1; Length 113;  
Matches 35; Conservative 24; Mismatches 31; Indels 1; Gaps 1;

OY 2 TKLEHLEGIYINIFHOYSVRKGFHDTLSKGLKQLTKELANTIKNIK-DKAVIDEIFOG 60

DB 7 SOLERSSTIINVFHOYSRKYGHPDILKAEFKMVKDLPNFKRKRENNELLDIMED 66

OY 61 LDANODEQVDFEFLISVAIALKAAHYTHK 91

DB 67 LDTNODMQLSFEECMMLMGLKLIFFACHEKHE 97

## RESULT 11

S68242

calgranulin B - mouse

N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor

C:Species: Mus musculus (house mouse)

C:Date: 06-Sep-1996 #sequence\_revision 23-May-1997 #text\_change 22-Jun-1999

C:Accession: S68242; S68272

R:Tagase, E.; Weissman, I.L.

submitted to the EMBL Data Library, February 1992

A:Description: Mouse MRP8 and MRP14, two intracellular calcium-binding proteins associated

A:Reference number: S68242

A:Accession: S68242

A:Molecule type: mRNA

A:Residues: 1-113 <LAG>

A:Cross-references: EMBL:M83219; NID:g199807; PIDN:AA07228.1; PID:g199808

R:Rafferty, M.J.; Harrison, C.A.; Alewood, P.; Jones, A.; Geezy, C.L.

Biochem. J. 316, 285-293, 1996

A:Title: Isolation of the murine S100 protein MRP14 (14 kDa migration-inhibitory factor)

A:Reference number: S68272; MUID:96235204

A:Accession: S68272

A:Molecule type: protein

A:Residues: 2-10;95-109 <RAF>

A:Note: 107-His is identified as 3'-methylhistidine; the authors' source for the re

ylhistidine

C:Genetics:

A:Gene: MRP14

C:Complex: heterodimer and higher complexes with calgranulin A

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammato

F:2-113/Product: calgranulin B #status predicted <MAT>

F:11-45/Domain: calmodulin repeat homology <EP1>

F:55-87/Domain: calmodulin repeat homology <EP2>

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F:80-91/Disulfide bonds: #status experimental

F:103,105,107/Binding site: zinc (His) #status predicted

F:107/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 38.1%; Score 178.5; DB 1; Length 113;  
Best Local Similarity 39.6%; Pred. No. 2.1e-09;  
Matches 36; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

OY 2 TKLEHLEGIYINIFHOYSVRKGFHDTLSKGLKQLTKELANTIKNIK-DKAVIDEIFOG 60

DB 7 SOMERSITTIIDVFHOYSRKGFHDTLSKGFROMVBOALATPEKKEKREVALINDIMED 66

OY 61 LDANODEQVDFEFLISVAIALKAAHYTHK 91

DB 67 LDTNODMQLSFEECMMLMGLKLIFFACHEKHE 97

RESULT 12

S35985

S-100 protein alpha chain - weatherfish

C:Species: Misgurnus fossilis (weatherfish)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S35985

R:Ivanenkov, V.V.; Gerke, V.; Minin, A.A.; Pleissmann, U.; Weber, K.

Mech. Dev. 42, 151-158, 1993

A:Title: Transduction of Ca(2+) signals upon fertilization of eggs: identification

A:Reference number: S35985; MUID:94031845

A:Accession: S35985

A:Molecule type: protein

A:Residues: 1-95 <IWA>

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: calcium binding; EF hand

F:49-81/Domain: calmodulin repeat homology <EP2>

Query Match 37.9%; Score 177.5; DB 1; Length 95;  
Best Local Similarity 45.9%; Pred. No. 2.2e-09;  
Matches 39; Conservative 16; Mismatches 29; Indels 1; Gaps 1;

OY 1 MKLEHLEGIYINIFHOYSVRKGFHDTLSKGLKQLTKELANTIKNIKDKAVIDEIFOG 60

DB 1 VSQLESAMESLIKVFHYSSKEDKYLKRAELKSLLOGELNDFLSAKDPVYKIMSD 60

OY 61 LDANODEQVDFEFLISVAIALKAAH 85

DB 61 LDENODEQVDFEFLVLA-ALVVA 84

RESULT 13

A45135

profilaggrin - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Sep-1999

Biochim. Biophys. Acta 790, 164-173, 1984  
 A:Title: Purification, characterization and ion binding properties of human brain S100b  
 C:Reference number: A90653; PMID:85023393  
 A:Contents: annotation; metal ion-binding properties  
 C:Comment: This protein binds p53, tubulin and many other proteins at physiological concentrations  
 C:Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tightly than different affinities exist for both ions on each monomer. Physiological concentrations of zinc are in the range of 10<sup>-10</sup> M.  
 C:Comment: This protein is expressed predominantly in brain tissue by astroglial cells.  
 C:Comment: The homodimer contains disulfide bonds, but the bond pattern has not been determined.  
 C:Genetics:  
 A:Gene: GDB:S100B  
 A:Cross-references: GDB:120360; OMIM:176990  
 A:Map position: 21q22.3-21q22.3  
 A:Introns: 46/3  
 A:Note: the first intron occurs before the initiator codon  
 C:Complex: homodimer; heterodimer with S-100 protein alpha chain (see PIR:BCBU1A)  
 C:Superfamily: S-100 protein; calmodulin repeat homology  
 C:Keywords: blocked amino end; brain; calcium binding; EF hand; heterodimer; homodimer; S-100 protein; S-100 protein beta chain #status experimental <EF1>  
 F:19-22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted  
 F:62,64,66,68,73/Binding site: calcium (Asp, Asp, Asp, Glu, Glu) #status predicted  
 F:92/Product: S-100 protein repeat homology <EF1>  
 F:40/Domain: calmodulin repeat homology <EF2>  
 F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #status predicted  
 F:19,22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted  
 F:62,64,66,68,73/Binding site: calcium (Asp, Asp, Asp, Glu, Glu) #status predicted

Query Match 40.4%; Score 189; DB 1; Length 92;  
 Best Local Similarity 39.5%; Pred. No. 2e-10;  
 Matches 34; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

DB 1 MTKLEHLEGVNIFHOYSVRKGFDTLSKGLKLTREKATINIKKAVIDEIFOG 60  
 1 MSELERKAMVALIDVFHOYSRGEGRKRLKSELKELINNELSHLEIKRQEVVDKVMET 60

QY 61 LDANODEOVDFOEFLISLVAIALKAH 86  
 61 LDNDGDECDFOEFMAFVAVTATACH 86

Db 61 LDNDGDECDFOEFMAFVAVTATACH 86

RESULT 8  
 A26557  
 S-100 protein beta chain - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 25-Mar-1988 #sequence, revision 04-Nov-1994 #text, change 13-Aug-1999  
 C:Accession: A60046; S07357; A26557  
 R:Maeda, T.; Usui, H.; Araki, K.; Kuwano, R.; Takahashi, Y.; Suzuki, Y.  
 PNAS Res. Mol. Brain Res. 10, 193-202, 1991  
 A:Title: Structure and expression of rat S-100 beta subunit gene.  
 A:Reference number: A60046; PMID:91359841  
 A:Accession: A60046  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-92 <MAE>  
 A:Cross-references: GB:S53527  
 R:Kuwano, R.; Usui, H.; Maeda, T.; Fukui, T.; Yamamori, N.; Ohtsuka, E.; Ikehara, M.; Tanabe, T.  
 Nucleic Acids Res. 12, 7455-7465, 1984  
 A:Title: Molecular cloning and the complete nucleotide sequence of cDNA to mRNA for S-100 beta subunit.  
 A:Reference number: S07357; PMID:85037924  
 A:Accession: S07357  
 A:Molecule type: mRNA  
 A:Residues: 1-92 <KUU>  
 A:Cross-references: EMBL:X01090; NID:957174; PIDN:CAZ5567.1; PID:957175  
 R:Dunn, R.; Landry, C.; O'Hanlon, D.; Dunn, J.; Allaire, R.; Brown, I.; Marks, A.  
 J. Biol. Chem. 262, 3562-3566, 1987  
 A:Title: Reduction in S100 protein beta subunit mRNA in C6 rat glioma cells following treatment with retinoic acid.  
 A:Reference number: A26557; PMID:87137648  
 A:Accession: A26557  
 A:Molecule type: mRNA  
 A:Residues: 6-92 <DUU>  
 A:Cross-references: GB:M15705  
 C:Comment: S-100 protein occurs as alpha-beta heterodimers, alpha-alpha heterodimers, and C:Genetics:

A:Introns: 46/3  
 C:Superfamily: S-100 protein; calmodulin repeat homology  
 C:Keywords: brain; calcium binding; dimer; EF hand; zinc  
 F:2-92/Product: S-100 protein beta chain #status predicted <MAE>  
 F:6-40/Domain: calmodulin repeat homology <EF1>

Query Match 40.0%; Score 187; DB 2; Length 92;  
 Best Local Similarity 38.4%; Pred. No. 3e-10;  
 Matches 33; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 1 MTKLEHLEGVNIFHOYSVRKGFDTLSKGLKLTREKATINIKKAVIDEIFOG 60  
 1 MSELERKAMVALIDVFHOYSRGEGRKRLKSELKELINNELSHLEIKRQEVVDKVMET 60

DB 61 LDANODEOVDFOEFLISLVAIALKAH 86  
 61 LDNDGDECDFOEFMAFVAVTATACH 86

QY 61 LDANODEOVDFOEFLISLVAIALKAH 86  
 61 LDNDGDECDFOEFMAFVAVTATACH 86

Db 61 LDNDGDECDFOEFMAFVAVTATACH 86

RESULT 9  
 BCOBIB  
 S-100 protein beta chain - bovine  
 N:Alternate names: neurocalcin delta-binding protein S100-beta  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 31-May-1979 #sequence, revision 14-Nov-1983 #text, change 24-Nov-1999  
 R:Isobe, T.; Okuyama, T.  
 Eur. J. Biochem. 89, 379-388, 1978  
 A:Title: The amino-acid sequence of S-100 protein (PAP-I-b protein) and its relation to the S-100 protein family.  
 A:Reference number: A91254; PMID:79045265  
 A:Accession: A91254  
 A:Molecule type: protein  
 A:Residues: 1-91 <ISO>  
 A:Experimental source: brain  
 A:Note: this sequence has since been revised in reference A91110  
 R:Isobe, T.; Okuyama, T.  
 Eur. J. Biochem. 116, 79-86, 1981  
 A:Title: The amino-acid sequence of the alpha subunit in bovine brain S-100 a protein.  
 A:Reference number: A91110; PMID:81236562  
 A:Accession: A91110  
 A:Molecule type: protein  
 A:Residues: 1-91 <ISO>  
 R:Baudier, J.; Gerard, D.  
 Biochemistry 22, 3360-3366, 1983  
 A:Title: Ions binding to S100 proteins: structural changes induced by calcium and zinc.  
 A:Reference number: A90471; PMID:84000339  
 A:Contents: annotation; metal ion-binding properties  
 R:Marshak, D.R.; Umekawa, H.; Watterson, D.M.; Hidaka, H.  
 Arch. Biochem. Biophys. 240, 777-780, 1985  
 A:Title: Structural characterization of the calcium binding protein S100 from adipose tissue.  
 A:Reference number: A90075; PMID:85278169  
 A:Accession: A90075  
 A:Molecule type: protein  
 A:Residues: 1-91 <MAE>  
 A:Experimental source: adipose tissue  
 R:Okazaki, K.; Obara, N.H.; Inoue, S.; Hidaka, H.  
 Biochem. J. 306, 551-555, 1995  
 A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in brain.  
 A:Reference number: S54343; PMID:95194333  
 A:Accession: S54348  
 A:Molecule type: protein  
 A:Residues: 56-61, 'N', 63-79, 'V' <OKA>  
 C:Comment: The S-100 protein is composed of two related polypeptide chains, alpha and beta. The S-100 protein is also found in a variety of other tissues.  
 C:Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc more tightly than different affinities exist for both ions on each monomer. Physiological concentrations of zinc are in the range of 10<sup>-10</sup> M.  
 C:Superfamily: S-100 protein; calmodulin repeat homology  
 C:Keywords: blocked amino end; brain; calcium binding; EF hand; zinc  
 F:5-39/Domain: calmodulin repeat homology <EF1>  
 F:48-80/Domain: calmodulin repeat homology <EF2>  
 F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental



C:Keywords: calcium binding; EF hand; monomer; neutrophil; zinc  
 F:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>  
 F:6-39/Domain: calmodulin repeat homology <EF1>  
 F:49-81/Domain: calmodulin repeat homology <EF2>  
 F:66-90/Region: zinc binding #status predicted

Query Match 100.0%; Score 468; DB 2; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 2e-35;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNKRAVIDEIFOG 60  
 DB 1 MTKLEHLEGIIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNKRAVIDEIFOG 60

OY 61 LDANODEQVDFEFTSLVAIALKAHYHTKE 92  
 DB 61 LDANODEQVDFEFTSLVAIALKAHYHTKE 92

ILT 2  
 .406

calgranulin c - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 23-May-1997

C:Accession: A55406  
 R:Del1/Angelica, E.C.; Schleicher, C.H.; Santone, J.A.

J. Biol. Chem. 269, 28929-28936, 1994

A:Title: Primary structure and binding properties of calgranulin C, a novel S100-like ca  
 A:Reference number: A55406; MUID:95050708

A:Accession: A55406

A>Status: preliminary

A:Molecule type: protein

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: calcium binding; EF hand

F:48-80/Domain: calmodulin repeat homology <EF2>

Query Match 70.9%; Score 332; DB 2; Length 91;  
 Best Local Similarity 70.3%; Pred. No. 3e-23;

Matches 64; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 2 TKLEHLEGIIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNKRAVIDEIFOG 61  
 DB 1 TKLEHLEGIIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNKRAVIDEIFOG 60

OY 62 DANODEQVDFEFTSLVAIALKAHYHTKE 92  
 DB 61 DANODEQVDFEFTSLVAIALKAHYHTKE 91

RESULT 3

A42628

calgranulin B - bovine (fragment)

N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory facto  
 in 2

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1993 #sequence\_revision 23-May-1997 #text\_change 23-May-1997

C:Accession: B22309; A42628

R:Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,

submitted to the Protein Sequence Database, July 1992

A:Reference number: A22309

A:Accession: B22309

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-122 <72N>

R:Danoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignals, P.V.

Biochemistry 31, 5898-5905, 1992

A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil

A:Reference number: A42628; MUID:92304974

A:Accession: A42628

A:Molecule type: protein

A:Residues: 4-32, 'F', 34-56 <DIA>  
 C:Complex: heterodimer and higher complexes with calgranulin A  
 C:Superfamily: S-100 protein; calmodulin repeat homology  
 C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation;  
 F:6-40/Domain: calmodulin repeat homology <EF1>  
 F:50-82/Domain: calmodulin repeat homology <EF2>

Query Match 48.4%; Score 226.5; DB 1; Length 122;  
 Best Local Similarity 51.6%; Pred. No. 1.2e-13;  
 Matches 47; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

OY 1 MTKLEHLEGIIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNKRAVIDEIFOG 59  
 DB 1 MSOMESIETIINIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNKRAVIDEIFOG 60

OY 60 GLDANODEQVDFEFTSLVAIALKAHYHTKE 90  
 DB 61 DLDNDVKQLSFEFTSLVAIALKAHYHTKE 91

RESULT 4

B31848

calgranulin B [validated] - human

N:Alternate names: calcium-binding protein MRP-14; cystic fibrosis-associated antly-  
 (MRP-14); MIF-related 14K protein; S-100 calcium-binding protein A9 (S100A9)

C:Species: Homo sapiens (man)

C:Date: 21-May-1990 #sequence\_revision 23-May-1997 #text\_change 08-Dec-2000

C:Accession: B31848; S00667; A3819; B60911; B61082; D54327

R:Agasse, E.; Clerc, R.G.;

Mol. Cell. Biol. 8, 2402-2410, 1988

A:Title: Cloning and expression of two human genes encoding calcium-binding protein

A:Reference number: A93102; MUID:88302148

A:Accession: B31848

A:Molecule type: DNA

A:Residues: 1-114 <AG>

A:Cross-references: GB:M21064; NID:918689; PIDN:AAA6326.1; PID:9386958

R:Odink, K.; Cerletti, N.; Brueggem, J.; Clerc, R.G.; Tarsesay, L.; Zwadlo, G.; Gerh.

Nature 330, 80-82, 1987

A:Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthr

A:Reference number: S00667; MUID:88039099

A:Accession: S00667

A:Molecule type: mRNA

A:Residues: 1-114 <ODI>

A:Cross-references: EMBL:X06233; NID:934770; PIDN:CAA29579.1; PID:934771

A:Note: parts of this sequence were confirmed by protein sequencing

R:Murro, S.; Collart, F.R.; Huberman, E.

J. Biol. Chem. 264, 8356-8360, 1989

A:Title: A protein containing the cystic fibrosis antigen is an inhibitor of protei

A:Reference number: A33819; MUID:8925276

A:Accession: A33819

A:Molecule type: mRNA

A:Residues: 1-114 <MUR>

A:Cross-references: GB:M26111; NID:986219; PIDN:AAA68480.1; PID:9516621

A:Note: part of this sequence was confirmed by protein sequencing; the amino end of

R:Andersen, K.B.; Sletten, K.; Berntzen, H.B.; Dale, I.; Brandtzeeg, P.; Jellum, E

Scand. J. Immunol. 28, 241-245, 1988

A:Title: The leucocyte I1 protein: identity with the cystic fibrosis antigen and th

A:Reference number: A60911; MUID:88321575

A:Accession: B60911

A:Molecule type: protein

A:Residues: 39-42, 'X', 44-50, 64-77, 'X', 79, 84, 'X', 86-90, 'X', 92-94, 'X', 96-98 <AND>

R:Toke, T.; Murakami, K.; Tomita, M.; Nozawa, R.

Chem. Pharm. Bull. 37, 1576-1580, 1989

A:Title: Amino acid sequences of 6088 antigens induced in HL-60 cells by 1,25-dihyd

A:Reference number: A61082; MUID:89376638

A:Accession: B61082

A:Molecule type: protein

A:Residues: 5-77, 80-90, 'A', 92-114 <TOB>

A:Note: the blocked amino end of the mature protein is identified as 2-Thr; residue

R:Madson, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Dejgaard, K.; Olsen, E.; K.

J. Invest. Dermatol. 97, 701-712, 1991

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 8, 2001, 15:03:05 ; Search time 14.33 Seconds

(without alignments)  
441.208 Million cell updates/sec

Title: US-09-227-854-2

Sequence: 1 MKLEHEHLEGIYVIFHQYV.....EFISLVALKKAHTHTKE 92

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

11 number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.67:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	468	100.0	92 2 JC4712	S-100 calcium-bind
2	332	70.9	91 2 A55406	calgranulin C - pi
3	226.5	48.4	122 1 A42628	calgranulin B - bo
4	214.5	45.8	114 1 B31848	calgranulin B [val
5	194	41.5	95 2 S24146	S-100 protein P -
6	190	40.6	92 2 A48015	S-100 protein beta
7	189	40.4	92 1 BCH01B	S-100 protein beta
8	187	40.0	92 2 A26557	S-100 protein beta
9	185	39.5	91 1 BCH01B	S-100 protein beta
10	180.5	38.6	113 1 JN0686	calgranulin B - ra
11	178.5	38.1	113 1 S68242	calgranulin B - mo
12	177.5	37.9	95 1 S35985	S-100 protein alpha
13	168	35.9	591 2 A45135	profilaggrin - hum
14	167	35.7	102 1 JQ1300	calgizazarin - rabb
15	163.5	34.9	101 2 S06207	calvasculin - mus
16	162.5	34.7	94 1 BCH01A	S-100 protein alpha
17	161.5	34.5	94 1 BCH01A	S-100 protein alpha
18	160.5	34.3	101 2 S01759	calvasculin - rat
19	158	33.8	93 1 BCH0CF	calvasculin A [val
20	157.5	33.7	101 2 A48219	calvasculin - huma
21	157	33.5	105 1 I37080	calgizazarin - huma
22	156	33.3	306 2 A48118	major epidermal ca
23	154	32.9	89 1 I56163	calgranulin A - mo
24	153.5	32.8	98 2 A41988	S-100 calcium-bind
25	152.5	32.6	100 2 A53217	placental calcium-
26	149	31.8	89 1 JN0685	calgranulin A - ra
27	147.5	31.5	90 1 BCH0Y	calgizazarin - huma
28	147.5	31.5	97 2 A30129	S-100 protein, lun
29	146	31.2	110 2 B48219	S-100 calcium-bind

30	144.5	30.9	217 2 JEO330	26-kDa Ca2+-bindin
31	142.5	30.4	89 2 A54314	calgizazarin - mouse
32	142.5	30.4	90 1 S27011	calgizazarin - rabbit
33	139.5	29.8	90 2 B28363	calgizazarin - rat
34	139	29.7	99 2 S20342	calgizazarin - pr
35	137.5	29.4	98 2 JCS064	S-100 calcium-bind
36	136	29.1	65 2 A41004	calgizazarin - chic
37	127.5	27.2	95 1 LUPG10	calgizazarin I light
38	127.5	27.2	97 1 JH0663	calgizazarin I light
39	127.5	27.2	97 2 JCI139	calgizazarin I light
40	127.5	27.2	97 2 B28489	calgizazarin I light
41	126.5	27.0	97 2 A28489	calgizazarin I light
42	124	26.5	79 1 KLBO1	calgizazarin I light
43	123.5	26.4	95 2 A31373	calgizazarin I light
44	122.5	26.2	79 1 KLBO1	calgizazarin I light
45	121.5	26.0	79 1 JN0246	calgizazarin I light

#### ALIGNMENTS

RESULT 1  
JC4712  
S-100 calcium-binding protein A12 - human  
N:Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; utrophin protein  
C:Species: Homo sapiens (man)  
C:Date: 10-May-1996 #sequence, revision 19-Jul-1996 #text\_change 13-Aug-1999  
C:Accession: JC4712; JC4717; JC4891; S56113; S56114  
R:Yamamura, T.; Hittom, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Salto, S.; Tsu  
Biochem. Biophys. Res. Commun. 221, 356-360, 1996  
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome map  
A:Reference number: JC4712; MUID:96192053  
A:Accession: JC4712  
A:Molecule type: mRNA  
A:Residues: 1-92 <YAM>  
A:Cross-references: DDBJ:DB3657; NID:G1502284; PIDN:BAI2030.1; PID:G1502285  
R:Marl, T.; Ertmann, K.D.; Gallin, M.Y.  
Biochem. Biophys. Res. Commun. 221, 454-458, 1996  
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequ  
A:Reference number: JC4717; MUID:96192069  
A:Accession: JC4717  
A:Molecule type: protein  
A:Residues: 2-92 <MAR>  
A:Experimental source: Onchocerca volvulus infecting human tissue  
R:Ilig, E.C.; Troxler, H.; Buerigler, D.M.; Kuster, T.; Markert, M.; Guignard, F.;  
Biochem. Biophys. Res. Commun. 225, 146-150, 1996  
A:Title: Amino acid sequence determination of human S100 A12 (p6, Calgranulin C, CG  
A:Reference number: JC4891; MUID:96352419  
A:Accession: JC4891  
A:Molecule type: protein  
A:Residues: 2-92 <ILIG>  
R:Guignard, F.; Manuel, J.; Markert, M.  
Biochem. J. 309, 395-401, 1995  
A:Title: Identification and characterization of a novel human neutrophil protein re  
A:Reference number: S56113; MUID:95351965  
A:Accession: S56113  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 'XX', 4-14, 'Y', 16-17, 'XXX', <GU1>  
A:Experimental source: Isoform 6a  
A:Accession: S56114  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 2-21 <GU12>  
A:Experimental source: Isoform 6b  
C:Comment: This protein is released by activated neutrophils in the course of infla  
C:Gene: GDB:S100A12; p6; MRP6; CGRP; CAAF1  
A:Cross-references: GDB:S5218374  
A:Map position: 1921-1921  
C:Complex: monomer  
C:Superfamily: S-100 protein; calmodulin repeat homology



```

CC ONE ALPHA AND ONE BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X01090; CAA25567.1; -.
DR EMBL: M54919; AAA42096.1; -.
DR EMBL: S53527; -. NOT_ANNOTATED_CDS.
DR EMBL: S53522; -. NOT_ANNOTATED_CDS.
DR EMBL: M15705; -. NOT_ANNOTATED_CDS.
DR PIR: S07357; S07357.
DR PIR: A26557; A26557.
DR PDB: 1SYM; 07-DEC-96.
DR PDB: 1QK; 11-NOV-98.
DR PDB: 1B4C; 30-DEC-98.
DR InterPro: IPR001751; -.
DR InterPro: IPR002048; -.
DR Pfam: PF01023; S_100; 1.
DR Pfam: PF00036; efhand; 1.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
DR Calcium-binding; zinc; Metal-binding; 3D-structure.
FT INT_MET 0
FT CA_BIND 18 31 SITE I (LOW AFFINITY).
FT CA_BIND 61 72 SITE II (HIGH AFFINITY).
SQ SEQUENCE 91 AA; 10613 MW; 2378AA8B8FF7134D CRC64;

Query Match 38.9%; Score 182; DB 1; Length 91;
Best Local Similarity 37.6%; Pred. No. 7.3e-11;
Matches 32; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 2 TKLEHLEGIIVNIFHOYSVRKRGHDTLSKGLKQLTKRELANTIKNIKRAVIDEFG 61
DB 1 SELEKAMVALIDVFHOYSRGREGDKHKLKLSKELINNELSHFLEIKEDYVDKMETL 60

QY 62 DANODEQVDFOEFTSLVAIALKAH 86
61 DEDGDGECDFOEFMAFVSMVTACH 85

RESULT 15
S109_RAT STANDARD; PRT; 113 AA.
ID S109_RAT
AC P50116;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CALGRANULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)
DE (MRP-14).
OS S100A9 OR MRP14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=LEWIS/N; TISSUE=peritoneal cavity;
RX MEDLINE=93343942; PubMed=8343166;
RA Imamiichi T., Uchida I., Wahl S.M., McCartney-Francis N.;
RT "Expression and cloning of migration inhibitory factor-related
RT protein (MRP)8 and MRP14 in arthritis-susceptible rats.";
RL Biochem. Biophys. Res. Commun. 194:819-825(1993).

```

```

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L18948; AAA18214.1; -.
DR HSSP: P04271; 1UW0.
DR InterPro: IPR001751; -.
DR InterPro: IPR002048; -.
DR Pfam: PF01023; S_100; 1.
DR Pfam: PF00036; efhand; 1.
DR PROSITE: PS00018; EF_HAND; FALSE_NEG.
DR PROSITE: PS00303; S100_CABP; 1.
DR Calcium-binding.
FT CA_BIND 24 37 SITE I (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 68 79 SITE II (HIGH AFFINITY) (POTENTIAL).
SQ SEQUENCE 113 AA; 13214 MW; 993A0044A7AECAFB CRC64;

Query Match 38.6%; Score 180.5; DB 1; Length 113;
Best Local Similarity 38.5%; Pred. No. 1.3e-10;
Matches 35; Conservative 24; Mismatches 31; Indels 1; Gaps 1;

QY 2 TKLEHLEGIIVNIFHOYSVRKRGHDTLSKGLKQLTKRELANTIKNIK-DRVIDEFG 60
DB 7 SQLEKSTLIINVFHOYSRGHDTLNKAEFKEMVKDLPNFKRKRRNELLRIDMED 66

QY 61 LDANODEQVDFOEFTSLVAIALKAHHTK 91
DB 67 LDTNODNQLSFEKCMMLMGLRIFACHEKLEH 97

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Search completed: June 8, 2001, 15:04:33  
Job time: 88 sec

RX MEDLINE-85291729; PubMed-4031854;  
 RA Jensen R., Marshak D.R., Anderson C., Lukas T.J., Matterson D.M.;  
 RT "Characterization of human brain S100 protein fraction: amino acid  
 sequence of S100 beta";  
 RL J. Neurochem. 45:700-705(1985);  
 RN (3)  
 RP METAL ION-BINDING PROPERTIES.  
 RA MEDLINE-85023393; PubMed-6487634;  
 RX Baudier J., Glasser N., Haglid K., Gerard D.;  
 RT "Purification, characterization and ion binding properties of human  
 brain S100B protein";  
 RL Biochim. Biophys. Acta 790:164-173(1984).  
 RN (4)  
 RP STRUCTURE BY NMR.  
 RA MEDLINE-98179937; PubMed-9519411;  
 RX Smith S.P., Shaw G.S.;  
 RT "A novel calcium-sensitive switch revealed by the structure of human  
 S100B in the calcium-bound form";  
 RL Structure 6:211-222(1998).  
 CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-  
 DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH  
 IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM  
 ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY  
 AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR  
 ONE ALPHA AND ONE BETA CHAIN.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE  
 BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.  
 CC -1- MISCELLANEOUS: IN ADDITION TO METAL-ION BINDING, THIS PROTEIN IS  
 INVOLVED WITH THE REGULATION OF PROTEIN PHOSPHORYLATION IN BRAIN  
 TISSUE.  
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
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 CC -----  
 DR EMBL; M59488; AAA60367.1; -;  
 DR EMBL; M59487; AAA60367.1; JOINED.  
 DR PIR; A03076; BCHUB.  
 DR PIR; A38364; A38364.  
 DR PDB; 1UW0; 10-JUN-98.  
 DR MIM; 176990; -;  
 DR InterPro; IPR001751; -;  
 DR InterPro; IPR002048; -;  
 DR Pfam; PF01023; S.100; 1.  
 DR Pfam; PF00036; efhand; 1.  
 DR PROSITE; PS00018; EF\_HAND; 1.  
 DR PROSITE; PS00303; S100\_CAMP; 1.  
 DR Calcium-binding; zinc; Metal-binding; 3D-structure.  
 DR INT\_MET 0 0  
 DR MOD\_RES 1 1 BLOCKED.  
 DR CA\_BIND 18 31 SITE I (LOW AFFINITY).  
 DR CA\_BIND 61 72 SITE II (HIGH AFFINITY).  
 DR SEQUENCE 91 AA; 10562 MW; 2378AA8B8FEA9F6 CRC64;  
 SQ  
 Query Match 39.3%; Score 184; DB 1; Length 91;  
 Best Local Similarity 38.8%; Pred. NO. 4.7e-11;  
 Matches 33; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

Db 61 DNDGDCDFQEFMAFVAMVTACH 85  
 RESULT 14  
 ID S10B\_RAT STANDARD: PRT: 91 AA.  
 AC P04631;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE S-100 PROTEIN, BETA CHAIN.  
 GN S100B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid-10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-85037924; PubMed-6093041;  
 RA Kuwano R., Usui H., Maeda T., Fukui T., Yamamori N., Ohtsuka E.,  
 RA Ikehara M., Takahashi Y.;  
 RT "Molecular cloning and nucleotide sequences of cDNA and genomic DNA  
 for alpha and beta subunits of S100 protein";  
 RL Nucleic Acids Res. 12:7455-7465(1984).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Kuwano R., Usui H., Maeda T., Kurihara T., Yamakuni T.,  
 RA Ohtsuka E., Ikehara M., Takahashi Y.;  
 RT "Molecular cloning and nucleotide sequences of cDNA and genomic DNA  
 for alpha and beta subunits of S100 protein";  
 RL Tanaguchi Symp. Brain Sci. 19:243-255(1987).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91359841; PubMed-1653388;  
 RA Maeda T., Usui H., Araki K., Kuwano R., Takahashi Y., Suzuki Y.;  
 RT "Structure and expression of rat S-100 beta subunit gene";  
 RL Brain Res. Mol. Brain Res. 10:193-202(1991).  
 RN (4)  
 RP SEQUENCE OF 5-91 FROM N.A.  
 RX MEDLINE-87137648; PubMed-3818655;  
 RA Dunn R., Landry C., O'Hanlon D., Dunn J., Alliore R., Brown I.,  
 RA Marks A.;  
 RT "Reduction in S100 protein beta subunit mRNA in C6 rat glioma cells  
 following treatment with anti-microtubular drugs";  
 RL J. Biol. Chem. 262:3562-3566(1987).  
 RN (5)  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-96387197; PubMed-8794737;  
 RA Drohat A.C., Amburgey J.C., Abildgaard F., Starich M.R.,  
 RA Baldisseri D.M., Weber D.J.;  
 RT "Solution structure of rat apo-S100B(beta beta) as determined by NMR  
 spectroscopy";  
 RL Biochemistry 35:11577-11588(1996).  
 RN (6)  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-98153156; PubMed-9485423;  
 RA Drohat A.C., Baldisseri D.M., Rustandi R.R., Weber D.J.;  
 RT "Solution structure of calcium-bound rat S100B(beta beta) as  
 determined by nuclear magnetic resonance spectroscopy";  
 RL Biochemistry 37:2729-2740(1998).  
 RN (7)  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-99226808; PubMed-10211826;  
 RA Drohat A.C., Tjandra N., Baldisseri D.M., Weber D.J.;  
 RT "The use of dipolar couplings for determining the solution structure  
 of rat apo-S100B";  
 RL Protein Sci. 8:800-809(1999).  
 CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-  
 DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH  
 IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM  
 ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY  
 AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.  
 CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR

RT "Spectral studies on the cadmium-ion-binding properties of bovine  
RT brain S-100b protein.";  
RL Biochem. J. 276:13-18(1991).  
RN [6]  
RP STRUCTURE BY NMR.  
RX MEDLINE-96398693; PubMed-8805590;  
RA Kildy P.M., van Eldik L.J., Roberts G.C.K.;  
RT "The solution structure of the bovine S100b protein dimer in the  
RT calcium-free state."  
CC Structure 4:1041-1052(1996).  
CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY.  
CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH  
CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM  
CC ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY  
CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.  
CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR  
CC ONE ALPHA AND ONE BETA CHAIN.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE  
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.  
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
CC PIR: A03077; BCB01B.  
CC PDB: ICFP; 12-MAR-97.  
CC PDB: IMHO; 18-NOV-98.  
CC InterPro: IPR001751;  
CC InterPro: IPR002048;  
CC Pfam: PF01023; S\_100; 1.  
CC Pfam: PF00036; efhand; 1.  
CC DR PROSITE: PS00018; EF\_HAND; 1.  
CC DR PROSITE: PS00303; S100\_CABP; 1.  
CC KW Calcium-binding; zinc; Metal-binding; Acetylation; 3D-structure.  
CC FT CA\_BIND 18 31 SITE I (LOW AFFINITY).  
CC FT CA\_BIND 61 72 SITE II (HIGH AFFINITY).  
CC FT SEQUENCE 91 AA: 10537 MW; 386201933DEB93A CRC64;  
SQ

Query Match 39.5%; Score 185; DB 1; Length 91;  
Best Local Similarity 38.8%; Pred. No. 3.8e-11;  
Matches 33; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

QY 2 TKLEHLEGIYINPHQSVRKGFDTLSKGLKQLTKELANTIKNIKDKAVIDEIPLGL 61  
DB 1 SELEKAVALLIDVPHQSVRGKDKRLKSELKELINNELSHLEIKQEVVDKVMETL 60  
QY 62 DANDEQVDFQEFISLVAIALKAH 86  
DB 61 DSDGDGECDFQEFMAFVAMITACH 85

RESULT 12  
S10B\_MOUSE  
ID S10B\_MOUSE STANDARD: PRT; 91 AA.  
AC P50114;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE S-100 PROTEIN, BETA CHAIN.  
GN S100B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID-10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN-BALB/C;  
RX MEDLINE-93386628; PubMed-8376406;  
RA Jiang H., Shah S., Hilt D.C.;  
RT "Organization, sequence, and expression of the murine S100 beta gene.  
RT Transcriptional regulation by cell type-specific cis-acting  
RT regulatory elements."  
RL J. Biol. Chem. 268:20502-20511(1993).

CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY.  
CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH  
CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM  
CC ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY  
CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.  
CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR  
CC ONE ALPHA AND ONE BETA CHAIN.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE  
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES  
CC (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
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CC -----  
CC DR EMBL: L22144; AAA03075.1;  
CC DR HSSP: P04271; 1U00.  
CC DR MGP: MGI:98217; S100b.  
CC InterPro: IPR001751;  
CC InterPro: IPR002048;  
CC Pfam: PF01023; S\_100; 1.  
CC Pfam: PF00036; efhand; 1.  
CC DR PROSITE: PS00018; EF\_HAND; 1.  
CC DR PROSITE: PS00303; S100\_CABP; 1.  
CC KW Calcium-binding; zinc; Metal-binding;  
CC FT INIT\_MET 0 0 BY SIMILARITY.  
CC FT CA\_BIND 18 31 SITE I (LOW AFFINITY).  
CC FT CA\_BIND 61 72 SITE II (HIGH AFFINITY).  
CC FT SEQUENCE 91 AA: 10597 MW; 2378A8B8BE1C94D CRC64;  
SQ

Query Match 39.5%; Score 185; DB 1; Length 91;  
Best Local Similarity 38.8%; Pred. No. 3.8e-11;  
Matches 33; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

QY 2 TKLEHLEGIYINPHQSVRKGFDTLSKGLKQLTKELANTIKNIKDKAVIDEIPLGL 61  
DB 1 SELEKAVALLIDVPHQSVRGKDKRLKSELKELINNELSHLEIKQEVVDKVMETL 60  
QY 62 DANDEQVDFQEFISLVAIALKAH 86  
DB 61 DSDGDGECDFQEFMAFVAMITACH 85

RESULT 13  
S10B\_HUMAN  
ID S10B\_HUMAN STANDARD: PRT; 91 AA.  
AC P04271;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 20-MAR-1987 (Rel. 04, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE S-100 PROTEIN, BETA CHAIN.  
GN S100B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID-9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-90368757; PubMed-2394738;  
RA Allore R.J., Friend W.C., O'Hanlon D., Neilson K.M., Bauman R.,  
RA Dunn R.J., Marks A.;  
RT "Cloning and expression of the human S100 beta gene."  
RT J. Biol. Chem. 265:15537-15543(1990).  
RN [2]  
RP SEQUENCE.

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CC EMBL; X65614; CAA46566.1; -  
 DR PIR; S24146; S24146.  
 DR HSP; P02638; ICNP.  
 DR MIM; 600614; -  
 DR InterPro; IPR001751; -  
 DR InterPro; IPR002048; -  
 DR Pfam; PF01023; S.100; 1.  
 DR Pfam; PF00036; ehand; 1.  
 DR PROSITE; PS00018; EF\_HAND; FALSE\_NEG.  
 DR PROSITE; PS00303; S100\_CABP; 1.  
 KW Calcium-binding; Placenta.  
 FT CA\_BIND 19 32 SITE I (LOW AFFINITY).  
 FT CA\_BIND 62 73 SITE II (HIGH AFFINITY).  
 FT CONFLICT 32 32 E -> T (IN REF. 2).  
 FT CONFLICT 44 44 F -> E (IN REF. 2).  
 J SEQUENCE 95 AA; 10400 MW; 786BE63FEAC6C1 CRC64;

Query Match 41.5%; Score 194; DB 1; Length 95;  
 Best Local Similarity 45.1%; Pred. No. 5.7e-12;  
 Matches 41; Conservative 17; Mismatches 33; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIWIFPHOYSVRKGFDTLSKGEKQLTKELANTIKNIKDAVIDEFG 60  
 DB 1 MTELETAMGMIIDVFSRYSSEGSTOTLTGKELKVLMEKLPGLGKDKDAVDKLLKD 60  
 OY 61 LDANODEVDVDFEFISLVAATLKAHYTHK 91  
 DB 61 LDANODVDFEFISLVAATLKAHYTHK 91

RESULT 10  
 S101\_ICTPU STANDARD; PRT; 92 AA.

AC 091061;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE ICMACALCIN.  
 OS Ictalurus punctatus (Channel catfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Siluriformes; Ictaluridae; Ictalurus.  
 NCBI\_TaxID=7998;

AN SEQUENCE FROM N.A.  
 RC TISSUE-Olfactory epithelium;  
 RX MEDLINE=97038343; PubMed=883937;  
 RA Porta A.R., Bettini E., Bulakova O.I., Baker H., Danho W.,  
 RA Margolis F.L.;  
 RT "Molecular cloning of Ictacalcin: a novel calcium-binding protein  
 from the channel catfish, Ictalurus punctatus.";  
 RL Brain Res. Mol. Brain Res. 41:81-89(1996).  
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN CATFISH CALCIUM HOMEOSTASIS.  
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN EPITHELIAL CELLS OF OLFACTORY  
 CC ROSETE, BARBEL, SKIN AND GILL BUT NOT BRAIN OR MUSCLE.  
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL; U33273; AAB52610.1; -  
 DR HSP; P30801; ICNP.  
 DR InterPro; IPR001751; -  
 DR InterPro; IPR002048; -  
 DR Pfam; PF01023; S.100; 1.  
 DR Pfam; PF00036; ehand; 1.  
 DR PROSITE; PS00018; EF\_HAND; 1.  
 DR PROSITE; PS00303; S100\_CABP; 1.  
 KW Calcium-binding.  
 FT CA\_BIND 19 32 SITE I (LOW AFFINITY) (POTENTIAL).  
 FT CA\_BIND 62 73 SITE II (HIGH AFFINITY) (POTENTIAL).  
 J SEQUENCE 92 AA; 10021 MW; DBFE78657F921C58 CRC64;

Query Match 40.2%; Score 188; DB 1; Length 92;  
 Best Local Similarity 46.8%; Pred. No. 2e-11;  
 Matches 37; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIWIFPHOYSVRKGFDTLSKGEKQLTKELANTIKNIKDAVIDEFG 60  
 DB 1 MSDLQGMALLISTFHKYSKGEKDKCTLTGKELKDLTKELGAFGNCSDAATLDRIFND 60  
 OY 61 LDANODEVDVDFEFISLVA 79  
 DB 61 LDANODVDFEFISLVA 79

RESULT 11  
 S10B\_BOVIN STANDARD; PRT; 91 AA.

AC P02638;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE S-100 PROTEIN, BETA CHAIN.  
 GN S100B.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;

RP SEQUENCE.  
 RX MEDLINE=79045265; PubMed=710399;  
 RA Isobe T., Okuyama T.;  
 RT "The amino-acid sequence of S-100 protein (PAP I-b protein) and its  
 relation to the calcium-binding proteins.";  
 RL Eur. J. Biochem. 89:379-386(1978).  
 RN [2]  
 RP REVISIONS TO 1-4.  
 RX MEDLINE=81236562; PubMed=7250124;  
 RA Isobe T., Okuyama T.;  
 RT "The amino-acid sequence of the alpha subunit in bovine brain S-100a  
 protein.";  
 RL Eur. J. Biochem. 116:79-86(1981).  
 RN [3]

RP SEQUENCE.  
 RX MEDLINE=85278169; PubMed=4026304;  
 RA Marshak D.R., Umekawa H., Matterson D.M., Hidaka H.;  
 RT "Structural characterization of the calcium binding protein s100 from  
 adipose tissue.";  
 RL Arch. Biochem. Biophys. 240:777-780(1985).  
 RN [4]  
 RP METAL ION-BINDING PROPERTIES.  
 RX MEDLINE=84000339; PubMed=6615778;  
 RA Baudier J., Gerard D.;  
 RT "Ions binding to S100 proteins: structural changes induced by calcium  
 and zinc on S100a and S100b proteins.";  
 RL Biochemistry 22:3360-3369(1983).  
 RN [5]

RP CADMIUM-BINDING STUDIES.  
 RX MEDLINE=91248136; PubMed=2039467;  
 RA Donato H. Jr., Mani R.S., Kay C.M.;

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DR EMBL: X61200; NOT\_ANNOTATED\_CDS.  
 DR HSSP: P04271; IJMO.  
 DR InterPro: IPR001751; .  
 DR InterPro: IPR002048; .  
 DR Pfam: PF01023; S\_100; 1.  
 DR Pfam: PF00036; ehand; 1.  
 DR PROSITE: PS00018; EF\_HAND; 1.  
 DR PROSITE: PS00303; S100\_CABP; 1.  
 DR Calcium-binding.  
 DR CA\_BIND 29 42 SITE I (LOW AFFINITY) (POTENTIAL).  
 DR CA\_BIND 72 83 SITE II (HIGH AFFINITY) (POTENTIAL).  
 DR SEQUENCE 119 AA; 14065 MW; 2D268DAF6309AD7A CRC64;

Query Match 44.9%; Score 210; DB 1; Length 119;  
 Best Local Similarity 43.3%; Pred. No. 2.3e-13;  
 Matches 39; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

OY 1 MKLEHREGIVNIFPHQSVRGKHGDTLSKGLKLTKELENTININDKVIDEIRFG 60  
 DB 11 LSELEKADVIITDVHFQSRREGDKDTLRKEKLTLEKOLANYLKHVNOVSIDIFXD 70

OY 61 LDANODEVDYDFQEFISLVAIALKAHYHTH 90  
 DB 71 LDNNKDDQSLFGEVMLLIRVTVATHEHLH 100

RESULT 8  
 S109\_RABIT STANDARD; PRT; 118 AA.  
 ID S109\_RABIT  
 AC P50117;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CALGRAULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)  
 DE (MRP-14) (FRAGMENT).  
 GN S100A9 OR MRP-14.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 NP [1]  
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-Neutrophils;  
 RX MEDLINE=9635278; PubMed=8702688;  
 RA Yang Z., de Veer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,  
 RA Underwood J.R., Robinson H.C.;  
 RA "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-  
 RA calgranulin C when incubated with inorganic [35S]sulfate";  
 RL J. Biol. Chem. 271:19802-19809(1996).  
 RN [2]  
 RP SEQUENCE OF 45-82 FROM N.A.  
 RC STRAIN-NEW ZEALAND WHITE;  
 RX MEDLINE=94198229; PubMed=8148323;  
 RA Mori S., Goto K., Goto F., Mutakami K., Okawara S., Yoshinaga M.;  
 RA "Dynamic changes in mRNA expression of neutrophils during the course  
 RA of acute inflammation in rabbits.";  
 RL Int. Immunol. 6:149-156(1994).  
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
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DR EMBL: AF091849; AAC61771.1; .  
 DR EMBL: D17404; BAA04227.1; .  
 DR InterPro: IPR001751; .  
 DR InterPro: IPR002048; .  
 DR InterPro: IPR002395; .  
 DR Pfam: PF01023; S\_100; 1.  
 DR Pfam: PF00036; ehand; 1.  
 DR PRINTS: PR00334; KININOGEN.  
 DR PROSITE: PS00018; EF\_HAND; 1.  
 DR PROSITE: PS00303; S100\_CABP; 1.  
 DR Calcium-binding; Repeat.  
 DR NON\_TER 1 1  
 DR CA\_BIND 9 22 SITE I (LOW AFFINITY) (POTENTIAL).  
 DR CA\_BIND 53 64 SITE II (HIGH AFFINITY) (POTENTIAL).  
 DR DOMAIN 103 118 2 x 8 AA TANDEM REPEATS OF G-H-G-H-  
 G-H-S-H.  
 DR REPEAT 103 110 1.  
 DR REPEAT 111 118 2.  
 DR SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;

Query Match 43.1%; Score 201.5; DB 1; Length 118;  
 Best Local Similarity 50.0%; Pred. No. 1.4e-12;  
 Matches 41; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

OY 11 IVNIFHQSVRGKHGDTLSKGLKLTKELENTI-KNIKDAVIDEIRFGDANODECV 69  
 DB 1 IINIFHQSVRGKHGDTLSKGLKLTKELENTI-KNIKDAVIDEIRFGDANODECV 60

OY 70 DFOEFISLVAIALKAHYHTH 91  
 DB 61 SFEFVILMARLVHSHHEMRK 82

RESULT 9  
 S10E\_HUMAN STANDARD; PRT; 95 AA.  
 ID S10E\_HUMAN  
 AC P25815;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE S-100P PROTEIN.  
 GN S100P OR S100E.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 NP [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE-Placenta;  
 RX MEDLINE=92339442; PubMed=1633809;  
 RA Becker T., Gerke V., Kube E., Weber K.;  
 RA "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA  
 RA cloning, recombinant protein expression and Ca2+ binding  
 RA properties.";  
 RL Eur. J. Biochem. 207:541-547(1992).  
 RN [2]  
 RP SEQUENCE OF 1-91.  
 RC TISSUE-Placenta;  
 RX MEDLINE=92171935; PubMed=1540168;  
 RA Emoto Y., Kobayashi R., Akatsuka H., Hida H.;  
 RA "Purification and characterization of a new member of the S-100  
 RA protein family from human placenta.";  
 RL Biochem. Biophys. Res. Commun. 182:1246-1253(1992).  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.  
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
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Db 61 DLDTNADKQLSFEETIMLVARLTVASHEKH 91

RESULT 6

ID S109\_HUMAN STANDARD; PRT; 114 AA.

AC P06702;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CALGAMULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)

DE (MRP-14) (P14) (LEUKOCYTE LI COMPLEX HEAVY CHAIN) (S100 CALCIUM-BINDING PROTEIN A9).

GN S100A9 OR MRP14 OR CAGB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

PP SEQUENCE FROM N.A.

MEDLINE=88039099; Pubmed=3313057;

RA Odink K., Cerletti N., Bruggen J., Clerc R.G., Tarcsay L., Zvaldo G., Gerhards G., Schlegel R., Sorg C.;

RT "Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis."

RL Nature 330:80-82(1987).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=88302148; Pubmed=3405210;

RA Lagasse E., Clerc R.G.;

RT "Cloning and expression of two human genes encoding calcium-binding proteins that are regulated during myeloid differentiation."

RL Mol. Cell. Biol. 8:2402-2410(1988).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=89255276; Pubmed=2656677;

RA Murao S., Collart F.R., Huberman E.;

RT "A protein containing the cystic fibrosis antigen is an inhibitor of protein kinases."

RL J. Biol. Chem. 264:8356-8360(1989).

RN [4]

RP SEQUENCE FROM N.A.

RA Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.;

RT "Human gene for migration inhibitory factor-related protein 14 (MRP14), variant allele."

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RP [5]

RP SEQUENCE OF 84-114, AND PHOSPHORYLATION.

RX MEDLINE=90044075; Pubmed=2478889;

RA Edgeworth J., Freeman P., Hogg N.;

RT "Tonomycin-regulated phosphorylation of the myeloid calcium-binding protein p14."

RL Nature 342:189-192(1989).

RN [6]

RP SEQUENCE OF 11-19; 26-37 AND 94-107.

RX MEDLINE=93162043; Pubmed=1286667;

RA Rasmussen H.H., van Damme J., Puye M., Gesser B., Cells J.E., Vandekerckhove J.;

RT "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes."

RL Electrophoresis 13:960-969(1992).

CC -1- FUNCTION: EXPRESSED BY MACROPHAGES IN ACUTELY INFLAMMED TISSUES AND IN CHRONIC INFLAMMATIONS. SEEM TO BE AN INHIBITOR OF PROTEIN KINASES. ALSO EXPRESSED IN EPITHELIAL CELLS CONSTITUTIVELY OR INDUCED DURING DERMATOSES. MAY INTERACT WITH COMPONENTS OF THE INTERMEDIATE FILAMENTS IN MONOCYTES AND EPITHELIAL CELLS.

CC -1- MISCELLANEOUS: HAS BEEN SHOWN TO BIND CALCIUM.

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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CC -----

DR EMBL: X06233; CAA29579.1; -

DR EMBL: M21064; AAA6326.1; -

DR EMBL: M26311; AAA68480.1; -

DR EMBL: AF237581; AAF62536.1; -

DR EMBL: A12032; CAA01002.1; -

DR EMBL: A12032; CAA01004.1; -

DR PIR: B31848; B31848.

DR PIR: A33819; A33819.

DR HSSP: P02638; 1CFP.

DR Aarhus/Ghent-2DPAGE; 5007; IEF.

DR Aarhus/Ghent-2DPAGE; 6010; IEF.

DR Aarhus/Ghent-2DPAGE; 6013; IEF.

DR Aarhus/Ghent-2DPAGE; 7013; IEF.

DR MIM: 123886; -

DR InterPro: IPR001751; -

DR InterPro: IPR002048; -

DR Pfam: PF01023; S\_100; 1.

DR Pfam: PF00036; ehnd; 1.

DR PROSITE: PS00018; EF\_HAND; 1.

DR PROSITE: PS00303; S100\_CABP; 1.

KW Calcium-binding; Macrophage; Phosphorylation.

FT CA\_BIND 23 36 SITE I (LOW AFFINITY) (POTENTIAL).

FT CA\_BIND 67 78 SITE II (HIGH AFFINITY) (POTENTIAL).

FT MOD\_RES 113 113 PHOSPHORYLATION.

SO SEQUENCE 114 AA; 13242 MW; C3BE19729E14C078 CRC64;

Query Match 45 8%; Score 214.5; DB 1; Length 114;

Best Local Similarity 46.7%; Pred. No. 8.2e-14;

Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKLEHELEGIVIFPHQSVRKGFPTLSKGLKLTKELANTI-KNIKRAVIDEIRQ 59

DB 5 MSQLENIETIITFPHQSVKYLGHPTDNLNGEKEKELVRKDLQNLKKNENKAVIEHME 64

QY 60 GLDANODEQVDFQEFISLVAIALKAHYTHK 91

DB 65 DLDTNADKQLSFEETIMLVARLTVASHEKH 96

RESULT 7

ID M126\_CHICK STANDARD; PRT; 119 AA.

AC P28318;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE PROTEIN MRP-126.

OS Gallus gallus (Chicken).

DE Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LEHORN; TISSUE-Bone marrow;

RX MEDLINE=92195690; Pubmed=1549365;

RA Nakano T., Graf T.;

RT "Identification of genes differentially expressed in two types of v-myd-transformed avian myelomonocytic cells."

RL Oncogene 7:527-534(1992).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN V-MYB-TRANSFORMED MYELOMONOCYTIC CELLS.

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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FT INIT MET 0 0 BY SIMILARITY.  
 FT CA BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).  
 FT CA BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).  
 SQ SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Query Match 67.1%; Score 314; DB 1; Length 91;  
 Best Local Similarity 65.9%; Pred. No. 2.8e-23;  
 Matches 60; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 2 TKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKQLTKELANTIKRDKAVIDEIFQGL 61  
 DB 1 TKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKQLTKELANTIKRDKAVIDEIFQGL 60  
 QY 62 DANODEQVDFEISLVAIALKAHYHTRKE 92  
 DB 61 DADKGAVSFEFVLVSVRLTAHIDIHKE 91

LUT 4  
 L1 RABIT STANDARD; PRT; 81 AA.  
 AC 077791;

DT 15-JUL-1998 (Rel. 38, Created)  
 DT 15-JUL-1998 (Rel. 38, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CALGRANULIN C (CAGC) (FRAGMENT).  
 GN S100A12.  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;

RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-Neutrophils;  
 RX MEDLINE=96355278; PubMed=8702688;  
 RA Yang Z., Devere M.J., Gardner E.E., Devenish R.J., Handley C.J.,  
 RA Underwood J.R., Robinson H.C.,  
 RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-  
 calgranulin C when incubated with inorganic [35S]sulfate."  
 RL J. Biol. Chem. 271:19802-19809(1996).  
 CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC -1 SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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CC EMBL; AF091848; AAC61770.1;  
 DR InterPro: IPR001751;  
 DR InterPro: IPR002048;  
 DR Pfam: PF01023; S.100; 1.  
 DR Pfam: PF00036; ehnd; 1.  
 DR PROSITE: PS00018; EF\_HAND; 1.  
 DR PROSITE: PS00303; S100\_CABP; 1.  
 DR Calcium-binding; 1.  
 FT NON\_TER 1 1  
 FT CA\_BIND 8 21 SITE I (LOW AFFINITY) (BY SIMILARITY).  
 FT CA\_BIND 51 62 SITE II (HIGH AFFINITY) (BY SIMILARITY).  
 SQ SEQUENCE 81 AA; 9401 MW; 95E67A209180CB6 CRC64;

Query Match 58.3%; Score 273; DB 1; Length 81;  
 Best Local Similarity 64.2%; Pred. No. 1.8e-19;  
 Matches 52; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 12 VNIHFOYSVRKGFDTLSKGLKQLTKELANTIKRDKAVIDEIFQGLDANODEQVDF 71  
 DB 1 INIHFOYSVRKGFDTLSKGLKQLTKELANTIKRDKAVIDEIFQGLDANODEQVDF 60

QY 72 QEFISLVAIALKAHYHTRKE 92  
 DB 61 KEFISLVAIALKAHYHTRKE 81

RESULT 5  
 S109\_BOVIN STANDARD; PRT; 122 AA.  
 ID S109\_BOVIN  
 AC P28783;

DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CALGRANULIN B (NEUTROPHIL CYTOSOLIC 23 KDA PROTEIN) (P23) (BEE22)  
 DE (FRAGMENT).  
 GN S100A9.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 OX (1)

RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Oesophageal epithelium.  
 RX MEDLINE=93280230; PubMed=8505358;  
 RA Tang T.K., Hong T.M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J.,  
 RA Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.-C.,  
 RA Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;  
 RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal  
 RT antibody W2 specifically reacts with condensed nuclei of  
 RT differentiated superficial cells."  
 RL J. Cell Sci. 104:237-247(1993).  
 RN [2]

RP SEQUENCE OF 4-56.  
 RC TISSUE-Neutrophils;  
 RX MEDLINE=92304974; PubMed=1610833;  
 RA Dianoux A.-C., Stasia M.-T., Garin J., Gagnon J., Vignais P.V.;  
 RT "The 23-kilodalton protein, a substrate of protein kinase C, in  
 RT bovine neutrophil cytosol is a member of the S100 family."  
 RL Biochemistry 31:5898-5905(1992).  
 CC -1 SUBUNIT: DISULFIDE LINKED HETERODIMER OF A 7/11 KDA AND A 22/23  
 CC KDA SUBUNITS.

CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC; LOOSELY ASSOCIATED TO THE  
 CC CYTOSKELETON.  
 CC -1 TISSUE SPECIFICITY: FOUND ESSENTIALLY IN PHAGOCYTTIC CELLS.  
 CC -1 PFM: PHOSPHORYLATED BY PROTEIN KINASE C.  
 CC -1 MISCELLANEOUS: CONTAINS TWO CA(2+)-BINDING DOMAINS PER PROTEIN.  
 CC -1 SIMILARITY: BELONGS TO THE S-100 FAMILY.

CC -1 SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
 DR HSP; P02636; ICFP.  
 DR InterPro: IPR001751;  
 DR InterPro: IPR002048;  
 DR Pfam: PF01023; S.100; 1.  
 DR Pfam: PF00036; ehnd; 1.  
 DR PROSITE: PS00018; EF\_HAND; PARTIAL.  
 DR PROSITE: PS00303; S100\_CABP; 1.  
 DR Calcium-binding; Phosphorylation.  
 FT NON\_TER 1 1  
 FT CA\_BIND 19 32 SITE I (LOW AFFINITY) (POTENTIAL).  
 FT CA\_BIND 63 74 SITE II (HIGH AFFINITY) (POTENTIAL).  
 SQ SEQUENCE 122 AA; 13673 MW; F3CA8C4880BECDC CRC64;

Query Match 48.8%; Score 228.5; DB 1; Length 122;  
 Best Local Similarity 51.6%; Pred. No. 4.3e-15;  
 Matches 47; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKQLTKELANTIKRDKAVIDEIFQ 59  
 DB 1 MSQESSIEIIVNIFHOYSVRKGFDTLSKGLKQLTKELANTIKRDKAVIDEIFQ 60  
 QY 60 GLDANODEQVDFEISLVAIALKAHYHTR 90

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
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 CC -----  
 CC EMBL: X97859; CA66453.1; -  
 CC EMBL: X98288; CA66934.1; JOINED.  
 CC EMBL: X98289; CA66934.1; JOINED.  
 CC EMBL: X98290; CA66934.1; JOINED.  
 CC EMBL: X98289; CAB94792.1; -  
 CC EMBL: X98290; CAB94792.1; JOINED.  
 CC EMBL: D49549; BAA08497.1; -  
 CC EMBL: D83664; BAA12036.1; -  
 CC EMBL: D83657; BAA12030.1; -  
 CC HSSP: P02633; 1BOD.  
 CC MIM: 603112; -  
 CC InterPro: IPR001751; -  
 CC InterPro: IPR002048; -  
 CC Pfam: PF01023; S\_100; 1.  
 CC Pfam: PF00036; ehand; 1.  
 CC PROSITE: PS00018; EF\_HAND; FALSE\_NEG.  
 CC PROSITE: PS00303; S100\_CABP; 1.  
 CC Calcium-binding; zinc; Metal-binding.  
 CC INIT\_MET 0.  
 CC FT CA\_BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).  
 CC FT CA\_BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).  
 CC SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;  
 CC  
 CC Query Match 98.9%; Score 463; DB 1; Length 91;  
 CC Best Local Similarity 100.0%; Pred. No. 2,7e-37;  
 CC Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 2 TKLEHLEGIIVNIFHOYSVRKRGHPTLSKGLKLTRELANTIKNKAVIDEIFQGL 61  
 CC DB 1 TKLEHLEGIIVNIFHOYSVRKRGHPTLSKGLKLTRELANTIKNKAVIDEIFQGL 60  
 CC QY 62 DANODEQVDFEFISLVATAAKAAHYTHKE 92  
 CC DB 61 DANODEQVDFEFISLVATAAKAAHYTHKE 91  
 CC  
 CC LN 2  
 CC PIG STANDARD; PRT; 91 AA.  
 CC ID S112\_PIG  
 CC AC P80310;  
 CC DT 01-FEB-1994 (Rel. 28, Created)  
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 CC DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 CC DE CALGRANULIN C (CAGC).  
 CC GN S100A12.  
 CC OS Sus scrofa (Pig).  
 CC OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CC OX NCBI\_TaxID=9823;  
 CC RN [1]  
 CC RP TISSUE-Granulocyte;  
 CC RX MEDLINE=95050708; PubMed=7961855;  
 CC RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;  
 CC RT "Primary structure and binding properties of calgranulin C, a novel  
 CC 1100-11ke calcium-binding protein from pig granulocytes.";  
 CC J. Biol. Chem. 269:28929-28936(1994).  
 CC RL J. Biol. Chem. 269:28929-28936(1994).  
 CC -1- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN GRANULOCYTES WITH SMALL  
 CC AMOUNTS FOUND IN LYMPHOCYTES.  
 CC -1- MISCELLANEOUS: IN THE ABSENCE OF ZINC BINDS ONE CALCIUM ION PER  
 CC MOLECULE, IN THE PRESENCE OF ZINC BINDS TWO CALCIUM IONS PER

CC MOLECULE.  
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
 CC -----  
 CC HSSP: P02632; 1CB1.  
 CC InterPro: IPR001751; -  
 CC InterPro: IPR002048; -  
 CC Pfam: PF01023; S\_100; 1.  
 CC Pfam: PF00036; ehand; 1.  
 CC PROSITE: PS00018; EF\_HAND; FALSE\_NEG.  
 CC PROSITE: PS00303; S100\_CABP; 1.  
 CC Calcium-binding; zinc; Metal-binding.  
 CC FT CA\_BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).  
 CC FT CA\_BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).  
 CC SQ SEQUENCE 91 AA; 10614 MW; B4204461432DFCB CRC64;  
 CC  
 CC Query Match 70.9%; Score 332; DB 1; Length 91;  
 CC Best Local Similarity 70.3%; Pred. No. 5,7e-25;  
 CC Matches 64; Conservative 10; Mismatches 17; Indels 0; Gaps 0;  
 CC  
 CC QY 2 TKLEHLEGIIVNIFHOYSVRKRGHPTLSKGLKLTRELANTIKNKAVIDEIFQGL 61  
 CC DB 1 TKLEHLEGIIVNIFHOYSVRKRGHPTLSKGLKLTRELANTIKNKAVIDEIFQGL 60  
 CC QY 62 DANODEQVDFEFISLVATAAKAAHYTHKE 92  
 CC DB 61 DANODEQVDFEFISLVATAAKAAHYTHKE 91  
 CC  
 CC RESULT 3  
 CC S112\_BOVIN STANDARD; PRT; 91 AA.  
 CC ID S112\_BOVIN  
 CC AC P79105;  
 CC DT 01-NOV-1997 (Rel. 35, Created)  
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 CC DE CALGRANULIN C (CAGC) (CALCIUM-BINDING PROTEIN IN AMNIOTIC FLUID 1)  
 CC GN S100A12 OR CAAP1.  
 CC OS Bos taurus (Bovine).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC OC Bovidae; Bovinae; Bos.  
 CC OX NCBI\_TaxID=9913;  
 CC RN [1]  
 CC RP TISSUE-From N.A.  
 CC RX MEDLINE=96298783; PubMed=8718672;  
 CC RA Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,  
 CC RA Nagasaki K.;  
 CC RT "A novel calcium-binding protein in amniotic fluid, CAAP1: its  
 CC molecular cloning and tissue distribution.";  
 CC J. Cell Sci. 109:805-815(1996).  
 CC RL J. Cell Sci. 109:805-815(1996).  
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
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 CC -----  
 CC EMBL: D49548; BAA08496.1; -  
 CC HSSP: P02633; 1BOD.  
 CC InterPro: IPR001751; -  
 CC InterPro: IPR002048; -  
 CC Pfam: PF01023; S\_100; 1.  
 CC Pfam: PF00036; ehand; 1.  
 CC PROSITE: PS00018; EF\_HAND; FALSE\_NEG.  
 CC PROSITE: PS00303; S100\_CABP; 1.  
 CC Calcium-binding; zinc; Metal-binding.



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OM protein - protein search, using sw model

Run on: June 8, 2001, 15:03:05 ; Search time 9.57 Seconds

(without alignments)  
329.311 Million cell updates/sec

Title: US-09-227-854-2  
Perfect score: 468  
Sequence: 1 MTKLEHLEGIVNIFHOYSV.....EFISVAIAKAAHYHTRKE 92

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues  
1 number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463	98.9	91	1	S112_HUMAN
2	332	70.9	91	1	S112_PIG
3	314	67.1	91	1	S112_BOVIN
4	273	58.3	81	1	S112_RABIT
5	228.5	48.8	122	1	S109_BOVIN
6	214.5	45.8	114	1	S109_HUMAN
7	210	44.9	119	1	M126_CHICK
8	201.5	43.1	118	1	S109_RABIT
9	194	41.5	95	1	S10E_HUMAN
10	188	40.2	92	1	S10I_ICPNU
11	185	39.5	91	1	S10B_BOVIN
12	185	39.5	91	1	S10B_MOUSE
13	184	39.3	91	1	S10B_HUMAN
14	182	38.9	91	1	S10B_RAT
15	180.5	38.6	113	1	S109_RAT
16	178.5	38.1	112	1	S109_MOUSE
17	167	35.7	102	1	S11I_RABIT
18	164.5	35.1	93	1	S10A_RAT
19	164	35.0	101	1	S11I_CHICK
20	163.5	34.9	101	1	S104_MOUSE
21	162.5	34.7	93	1	S10A_BOVIN
22	161.5	34.5	93	1	S10A_HUMAN
23	160.5	34.3	101	1	S10A_RAT
24	158	33.8	93	1	S108_HUMAN
25	157.5	33.7	101	1	S104_HUMAN
26	157	33.5	105	1	S11I_HUMAN
27	155.5	33.2	93	1	S10A_MOUSE
28	154	32.9	88	1	S10E_MOUSE
29	153.5	32.8	97	1	S10I_MOUSE
30	152.5	32.6	100	1	S102_BOVIN
31	149.5	31.9	92	1	S106_HORSE
32	149	31.8	88	1	S10E_RAT

ALIGNMENTS

RESULT ID	1	S112_HUMAN	STANDARD:	PRT:	91 AA.
AC	P80511:				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	CALGRANULIN C (CAGC) (P6) (CGRP) (NEUTROPHIL S100 PROTEIN) (CALCIUM-BINDING PROTEIN IN AMNIOTIC FLUID 1) (CAAF1) (P6).				
GN	S100A12.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
ON	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE-97138564; PubMed-9885590;				
RA	Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;				
RT	"Characterization of the human S100A12 (calgranulin C, p6, CAAF1, CGRP) gene, a new member of the S100 gene cluster on chromosome 1q21."				
RT	[2]				
RL	Cell Calcium 20:459-464(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE-96192053; PubMed-8619860;				
RA	Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E.,				
RT	Saito S., Tsukada T., Yamaguchi K.;				
RT	"Human CAAF1 gene -- molecular cloning, gene structure, and chromosome mapping."				
RL	Biochem. Biophys. Res. Commun. 221:356-360(1996).				
RN	[3]				
RP	SEQUENCE.				
RA	MEDLINE-96192069; PubMed-8619876;				
RA	Martl T., Ettmann K.D., Gallin M.Y.;				
RT	"Host-parasite interaction in human onchocerciasis: Identification and sequence analysis of a novel human calgranulin C."				
RL	Biochem. Biophys. Res. Commun. 221:454-458(1996).				
RN	[4]				
RP	SEQUENCE.				
RA	MEDLINE-96332419; PubMed-8769108;				
RA	Yig E.C., Troxler H., Buerigisser D.M., Kuster T., Markert M.,				
RT	Guignard F., Hunziker P., Birchler N., Heizmann C.W.;				
RT	"Amino acid sequence determination of human S100A12 (p6, calgranulin C, CGRP, CAAF1) by tandem mass spectrometry."				
RL	Biochem. Biophys. Res. Commun. 225:146-150(1996).				
RN	[5]				
RP	SEQUENCE OF 1-20.				
RA	MEDLINE-9551965; PubMed-7626002;				
RA	Guignard F., Maue J., Markert M.;				
RT	"Identification and characterization of a novel human neutrophil protein related to the S100 family."				
RL	Biochem. J. 309:395-401(1995).				
RN	[6]				
RP	SUBUNIT: MONOMER.				
CC	-1- TISSUE SPECIFICITY: MONOCYTES AND LYMPHOCYTES.				
CC	-1- MASS SPECTROMETRY: MW=10444; METHOD=ELECTROSPRAY.				

34	147.5	31.5	90	1	S106_HUMAN	P06703 homo sapien
35	147.5	31.5	97	1	S102_BOVIN	P10462 bos taurus
36	146	31.2	110	1	S105_HUMAN	P33763 homo sapien
37	142.5	30.4	89	1	S10E_MOUSE	P14069 mus musculu
38	142.5	30.4	90	1	S106_RABIT	P30801 oryctolagus
39	139.5	29.8	90	1	S106_RAT	P05964 rattus norv
40	139.5	29.8	92	1	S106_CHICK	O98953 gallus gall
41	139	29.7	99	1	S11I_PIG	P31950 sus scrofa
42	138.5	29.6	101	1	S107_BOVIN	O28050 bos taurus
43	137.5	29.4	98	1	S103_HUMAN	O99584 homo sapien
44	136	29.1	93	1	S105_MOUSE	O88945 mus musculu
45	131.5	28.1	102	1	S11X_HUMAN	O60417 homo sapien



OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MISTAR;  
 RA Konrad L., Gadius H.J., Annweiler G.;  
 RT "Sequence and expression study of calyculin in the rat testis."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ132717; CAB42002.1;  
 DR HSSP: P30801; IA03.  
 DR INTERPRO: IPR001751;  
 DR INTERPRO: IPR002048;  
 DR PFAM: PF00036; efnad: 1.  
 DR PFAM: PF01023; S\_100: 1.  
 DR PROSITE: PS00018; EF\_HAND; UNKNOWN\_1;  
 DR PROSITE: PS00303; S100\_CABP; 1.  
 DR Cyclic.  
 KW Cyclic.  
 SQ SEQUENCE 89 AA; 10035 MW; 2AA1A4163D57DC87 CRC64;

Query Match 29.8%; Score 139.5; DB 11; Length 89;  
 Best Local Similarity 43.8%; Pred. No. 6.4e-06;  
 Matches 35; Conservative 18; Mismatches 24; Indels 3; Gaps 2;  
 OY 4 LEEHLEGINIFHOYSVRKGHPTLSKGLKOLLTKELANTINIKDKAVIDEIFOGD 63  
 DB 5 LDOAIGLVAIFHKYSGKGDHRTLSKKELEKIQEL--TIGAKLQDAIARLMDLDR 62  
 OY 64 NODEQVDFOEFS-LVAIAL 82  
 DB 63 NKQDEVNFOEYVAFGLAL 82

RESULT 12  
 ID P79342 PRELIMINARY; PRT: 98 AA.  
 AC P79342;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE 8 KDA AMLEXANOX-BINDING PROTEIN.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Oyama Y., Shishibori T., Matsutomo M., Yamashita K., Maeta H.,  
 RT Kobayashi R.;  
 RT "Molecular cloning of a new 8kDa protein, isolated with Amlexanox  
 RT coupled column chromatography."  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB001567; BAA19411.1;  
 DR HSSP: P08206; IAAP.  
 DR INTERPRO: IPR001751;  
 DR INTERPRO: IPR002048;  
 DR PFAM: PF01023; S\_100: 1.  
 SQ SEQUENCE 98 AA; 11233 MW; 77858426025E643B CRC64;

Query Match 26.4%; Score 123.5; DB 6; Length 98;  
 Best Local Similarity 33.3%; Pred. No. 0.00021;  
 Matches 26; Conservative 20; Mismatches 29; Indels 3; Gaps 1;  
 OY 1 MTKLEHLEGINIFHOYSVRKGHPTLSKGLKOLLTKELANTINIKDKAVIDEIFOG 60  
 DB 6 LTELAKAITEVTTFTFFGRBGRKSLSVNEKELVTOQLPHL--LADVSLDEKMS 62  
 OY 61 LDANODEQVDFOEFSLV 78  
 DB 63 FVNDQSEIKFSEYRLI 80

RESULT 13  
 ID Q9UDP3 PRELIMINARY; PRT: 104 AA.  
 AC Q9UDP3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE WUSC: L\_NH0456N16.1 PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99063792; PubMed-9847074;  
 RA Sulston J.E., Waterston R.;  
 RT "Toward a complete human genome sequence."  
 RL Genome Res. 8:1097-1108(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA All J., Wohlmann P., Duckels G.;  
 RT "The sequence of Homo sapiens BAC clone RP11-456N16."  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.H.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC006379; AAD21786.1;  
 DR HSSP: P08206; IAAP.  
 DR INTERPRO: IPR001751;  
 DR INTERPRO: IPR002048;  
 DR PFAM: PF01023; S\_100: 1.  
 SQ SEQUENCE 104 AA; 11509 MW; 2316AEC84C9CF12A CRC64;

Query Match 25.7%; Score 120.5; DB 4; Length 104;  
 Best Local Similarity 32.9%; Pred. No. 0.00042;  
 Matches 26; Conservative 19; Mismatches 33; Indels 1; Gaps 1;  
 OY 8 LEGIYNIFHOYSVRKGHPTLSKGLKOLLTKELANTINIKDKAVIDEIFOGD 67  
 DB 14 IOLIAVFOKYGKNGYCNLSKTEFLSFMTLELAFTNORDPGLDM-KLDVSSDG 72  
 OY 68 QYDPOEFSLVAILKAAH 86  
 DB 73 QIDFFKFLNLIGGLAVACH 91

RESULT 14  
 ID Q9OVR5 PRELIMINARY; PRT: 83 AA.  
 AC Q9OVR5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE CALPROTECTIN LARGER COMPONENT MRP-14 (FRAGMENT).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95395365; PubMed-7665986;  
 RA Yui S., Mikami M., Yamazaki M.;  
 RT "Purification and characterization of the cytotoxic factor in rat  
 RT peritoneal exudate cells: its identification as the calcium binding  
 RT protein complex, calprotectin."  
 RL J. Leukoc. Biol. 58:307-316(1995).

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ID 09TV56 PRELIMINARY: PRT: 101 AA.
AC 09TV56;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE MEMASTASIN.
GN MTSI.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADIN-DUBRY; TISSUE=MADIN DABBY CANINE KIDNEY (MDCK);
RA Miyamoto H., Hasegawa K., Kim K., Sato H.;
RT "Expression of metastasis associated mtsi gene is co-induced with
RT membrane type-1 matrix metalloproteinase (MT1-MMP) during oncogenic
RT transformation and tubular formation of madin darby canine kidney
RT (MDCK) epithelial cells."
RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AB031064; BAA83419.1;
L INTERPRO: IPR001751;
DR INTERPRO: IPR002048;
DR PFAM: PF00036; etand; 1.
DR PFAM: PF01023; S.100; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE: PS00303; S100_CBP; 1.
SQ SEQUENCE 101 AA; 11847 MW; 5535387DB7577DF0 CRC64;

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Query Match 31.9%; Score 149.5; DB 6; Length 101;
Best Local Similarity 40.0%; Pred. No. 9.1e-07;
Matches 32; Conservative 21; Mismatches 24; Indels 3; Gaps 1;

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QY 4 LEFHLEGIYNIHQYSVKRGHDTLSKGLKQLTKELANTIKNKAVIDEIFQGLDA 63
DB 5 LEKALVWYVSTFKYSGKEDKFLNRSLEKELMELPSFLGKRDEAFAQKMSNIDS 64
QY 64 NDEQVDPQ---FISLVAI 80
DB 65 NRNDVEYQECYFELSCVAM 84

RESULT 9
QYH57 PRELIMINARY: PRT: 217 AA.
AC 09YH57;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE P26OLF.
GN P26OLF CDNA.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA MEDLINE=99008915; PubMed=9791000;
RA Miwa N., Kobayashi M., Takamatsu K., Kawamura S.;
RT "Purification and molecular cloning of a novel calcium-binding
RT protein, p26OLF, in the frog olfactory epithelium."
RL Blochem. Biophys. Res. Commun. 251:860-867(1998).
DR EMBL: D50333; BAA34388.1;
DR HSSP: P08206; 1A4P.
DR INTERPRO: IPR001751;
DR INTERPRO: IPR002048;
DR PFAM: PF01023; S.100; 2.
SQ SEQUENCE 217 AA; 24494 MW; 0403689A9E43810B CRC64;

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```

Query Match 30.9%; Score 144.5; DB 13; Length 217;
Best Local Similarity 32.2%; Pred. No. 6.2e-06;
Matches 29; Conservative 28; Mismatches 28; Indels 5; Gaps 2;

```

```

QY 2 TKLEHLEGIYNIHQYSVKRGHDTLSKGLKQLTKELANTIKNKD-KAYIDEIFQ- 59
DB 10 TEMERSMEKTIIVFORAGKEGNTSMNFEQFMNAELGSPKNOQDPAIRKIMKS 69
QY 60 ---GLDANODEQVDFQEFISLVAIALKAH 86
DB 70 VDGSGVQKQDGEIDPQEFELNLIGMAYACH 99

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RESULT 10
QYH57 PRELIMINARY: PRT: 495 AA.
AC 09UBG3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE TUMOR RELATED PROTEIN.
GN DRCL OR PDRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu Z.X., Wang M.R., Cai Y., Xu X., Han Y.L., Wang X.Q., Wu M.;
RT "Cloning and characterization of a novel gene associated with human
RT cancer."
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Xu Z.X., Wang M.R., Cai Y., Xu X., Han Y.L., Wang X.Q., Wu M.;
RT "Cloning and characterization of a novel cDNA associated with human
RT cancer."
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF185276; AAF00514.1;
DR EMBL: AF077831; AAD55747.1;
DR HSSP: P02633; 5ICB.
DR INTERPRO: IPR001751;
DR INTERPRO: IPR002048;
DR PFAM: PF00036; etand; 1.
DR PFAM: PF01023; S.100; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 495 AA; 53533 MW; CA882A11B4E64DC3 CRC64;

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```

Query Match 30.8%; Score 144; DB 4; Length 495;
Best Local Similarity 37.2%; Pred. No. 1.7e-05;
Matches 29; Conservative 21; Mismatches 28; Indels 0; Gaps 0;

```

```

QY 1 MKLEHLEGIYNIHQYSVKRGHDTLSKGLKQLTKELANTIKNKD-KAYIDEIFQ- 60
DB 1 MPOLLQNTIGTIEARRARKEGNTCTALTRELKRLLEQEPADVIVKPHDPADEVLR 60
QY 61 LDANODEQVDFQEFISLV 78
DB 61 LDEHGTGVEKFEFLV 78

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RESULT 11
QYH27 PRELIMINARY: PRT: 89 AA.
AC 09R27;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CALCYCLIN.
GN CACY.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

```



Query Match	40.48	Score 189	DB 13	Length 101
Best Local Similarity	43.28	Pred No. 2.2e-10		
Matches 41	Conservative 20	Mismatches 28	Indels 6	Gaps 2

RA Presland R.B., Haydock P.V., Fleckman P., Ntunusukstiri W., Dale B.A.  
RT "Characterization of the human epidermal profilaggrin gene. Genomic  
RT organization and identification of an S-100-like calcium binding

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2001, 15:03:05 ; Search time 19.35 Seconds

(Without alignments)  
557.268 Million cell updates/sec

Title: US-09-227-854-2

Sequence: 1 MTKLEHEGIVNIHFHOYSV.....EFISLVAIALKAHHTHKE 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

1 number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP:REMBL\_15:\*  
2: SP:archaea:\*  
3: SP:bacteria:\*  
4: SP:fungi:\*  
5: SP:human:\*  
6: SP\_invertebrate:\*  
7: SP\_mhc:\*  
8: SP\_mammal:\*  
9: SP\_organelle:\*  
10: SP\_phage:\*  
11: SP\_plant:\*  
12: SP\_podent:\*  
13: SP\_unclassified:\*  
14: SP\_vertebrate:\*  
15: SP\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	53.0	70	6 Q9TR16	Q9TR16 bos taurus
2	206.5	44.1	114	4 Q9NVM0	Q9NVM0 homo sapien
3	189	40.4	101	13 Q93395	Q93395 salicellus
4	186	39.7	92	13 Q9P8F6	Q9P8F6 ictalurus p
5	168	35.9	591	4 Q01720	Q01720 homo sapien
6	158	33.8	1218	4 Q05331	Q05331 homo sapien
7	154	32.9	79	11 Q9JL08	Q9JL08 mus musculu
8	149.5	31.9	101	6 Q9TV56	Q9TV56 canis famli
9	144.5	30.9	217	13 Q9YH57	Q9YH57 rana catesb
10	144	30.8	495	4 Q9UB63	Q9UB63 homo sapien
11	139.5	29.8	89	11 Q9R2B7	Q9R2B7 rattus norv
12	123.5	26.4	98	6 P79342	P79342 bos taurus
13	120.5	25.7	104	4 Q9UDP3	Q9UDP3 homo sapien
14	117.5	25.1	83	11 Q9OVR5	Q9OVR5 rattus sp.
15	112.5	24.0	73	6 Q28714	Q28714 onyctolagus
16	96	20.5	493	5 Q15872	Q15872 paramecium
17	95	20.3	473	10 Q9SE24	Q9SE24 oryza sativ
18	92.5	19.8	55	6 Q9TSB1	Q9TSB1 bos taurus
19	90	19.2	523	10 Q9SE25	Q9SE25 oryza sativ

20	89.5	19.1	535	10 Q38873	Q38873 arabidopsis
21	89	19.0	564	10 Q9ZRU9	Q9ZRU9 solanum tub
22	88.5	18.9	170	5 Q9NKV7	Q9NKV7 perlinope
23	87.5	18.7	226	10 Q81446	Q81446 arabidopsis
24	87.5	18.7	244	5 Q20804	Q20804 caenorhabd
25	85.5	18.3	162	5 Q9V315	Q9V315 drosophila
26	84.5	18.1	70	4 Q95663	Q95663 homo sapien
27	84.5	18.1	146	10 Q23480	Q23480 arabidopsis
28	84.5	18.1	167	4 Q9NZ08	Q9NZ08 homo sapien
29	84.5	18.1	167	6 Q9N1R1	Q9N1R1 bos taurus
30	84.5	18.1	167	11 Q9JLK6	Q9JLK6 mus musculu
31	84.5	18.1	226	6 Q9N1R0	Q9N1R0 bos taurus
32	84.5	18.1	227	4 Q9NZU7	Q9NZU7 homo sapien
33	84.5	18.1	227	11 Q9JLK7	Q9JLK7 mus musculu
34	83.5	17.8	163	11 Q9JLK5	Q9JLK5 mus musculu
35	83.5	17.8	216	11 Q9JLK4	Q9JLK4 mus musculu
36	83.5	17.8	248	10 Q65587	Q65587 arabidopsis
37	83	17.7	169	5 Q9NEM1	Q9NEM1 schistosoma
38	82.5	17.6	220	4 Q9NPM3	Q9NPM3 homo sapien
39	82.5	17.6	226	10 Q81447	Q81447 arabidopsis
40	82.5	17.6	571	10 Q48827	Q48827 arabidopsis
41	80	17.1	536	10 Q65644	Q65644 arabidopsis
42	79.5	17.0	163	6 Q9N1O9	Q9N1O9 bos taurus
43	79.5	17.0	553	10 Q80700	Q80700 arabidopsis
44	78.5	16.8	298	11 Q88751	Q88751 rattus norv
45	78.5	16.8	309	2 Q51695	Q51695 borrelia bu

## ALIGNMENTS

RESULT 1  
Q9TR16 PRELIMINARY; PRT; 70 AA.  
AC Q9TR16;  
DT 01-MAY-2000 (TREMREL\_13, Created)  
DT 01-MAY-2000 (TREMREL\_13, Last sequence update)  
DT 01-OCT-2000 (TREMREL\_15, Last annotation update)  
DE CORNER-ASSOCIATED ANTIGEN, CO-AG-CALGRANULIN C HOMOLOG.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP  
RA MEDLINE=96181454; Pubmed=8603881;  
RX Liu S.H., Gottsch J.D.;  
RT "Amino acid sequence of an immunogenic corneal stromal protein.";  
RL Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).  
DR HSPF; P02638; IMHO.  
DR INTERPRO; IPR001751;  
DR INTERPRO; IPR002048;  
DR PFAM; PF01023; S.100; 1.  
SQ SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;

Query Match 53.0%; Score 248; DB 6; Length 70;  
Best Local Similarity 68.6%; Pred. No. 6.1e-16;  
Matches 48; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 2 TKELEHEGIVNIHFHOYSVVRGHDLTLSKGLTKLLKELANTIKNKRAVIDEIOGL 61  
DB 1 TKLEDEHLEGINIFHOYSVVRGHDLTINKRELKLTREKLTONTKDDPTDIKIRODL 60  
QY 62 DANODEQVDF 71  
DB 61 DADKKAVVF 70  
RESULT 2  
Q9NVM0 PRELIMINARY; PRT; 114 AA.